

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 19:21:20 ; Search time 16 Seconds
(without alignments)
1176.655 Million cell updates/sec

Title: US-09-718-725A-125
Perfect score: 2198
Sequence: 1 MNKLCCALVFDISIKWT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*
1: /SID55/ptodata/1/pubpaa/US08_NEW_PUB.pep1.*
2: /SID55/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SID55/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SID55/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SID55/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /SID55/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
7: /SID55/ptodata/1/pubpaa/US09_NEW_PUB.pep1.*
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9: /SID55/ptodata/1/pubpaa/US11_NEW_PUB.pep1.*
10: /SID55/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
11: /SID55/ptodata/1/pubpaa/US11_NEW_PUB.pep1.*
12: /SID55/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2198	100.0	401	9 US-10-510-876-4	Sequence 4, Appli
2	2192	99.7	401	9 US-10-510-876-2	Sequence 2, Appli
3	2192	99.7	401	9 US-10-921-793-52	Sequence 52, Appli
4	2192	99.7	401	9 US-10-931-198-52	Sequence 52, Appli
5	2192	99.7	401	9 US-10-942-042-52	Sequence 52, Appli
6	2187	99.5	401	11 US-11-231-963-1	Sequence 1, Appli
7	2187	99.5	401	11 US-11-254-836-1	Sequence 1, Appli
8	2086	94.9	537	11 US-11-144-236-6	Sequence 6, Appli
9	2085	94.9	537	11 US-11-144-236-6	Sequence 1, Appli
10	1892	86.1	401	9 US-10-948-053-2	Sequence 2, Appli
11	1828	83.2	338	9 US-10-921-793-54	Sequence 54, Appli
12	1828	83.2	338	9 US-10-931-198-54	Sequence 54, Appli
13	1828	83.2	338	9 US-10-942-042-54	Sequence 54, Appli
14	1043	47.5	406	9 US-10-948-053-6	Sequence 6, Appli
15	1018	46.3	407	9 US-10-948-053-3	Sequence 3, Appli
16	1013.5	46.1	400	9 US-10-948-053-4	Sequence 4, Appli
17	1013.5	46.1	400	9 US-10-948-053-5	Sequence 5, Appli
18	1013	46.1	404	9 US-10-948-053-7	Sequence 7, Appli
19	1009	45.9	401	9 US-10-948-053-8	Sequence 8, Appli
20	945	43.0	161	11 US-11-154-257-3	Sequence 3, Appli
21	674	30.7	120	11 US-11-042-814-8	Sequence 8, Appli

22	444	20.2	300	11	US-11-154-257-2	Sequence 2, Appli
23	344	15.7	474	11	US-11-260-192-4	Sequence 4, Appli
24	332	15.1	235	11	US-11-126-126-16	Sequence 16, Appli
25	332	15.1	461	11	US-11-132-285-6	Sequence 6, Appli
26	332	15.1	461	11	US-11-182-945-4	Sequence 4, Appli
27	330	15.0	461	8	US-10-511-937-2945	Sequence 2945, App
28	330	15.0	461	9	US-10-523-328-5	Sequence 32, Appli
29	330	15.0	461	10	US-11-183-218-32	Sequence 32, Appli
30	330	15.0	461	11	US-11-183-205-32	Sequence 5, Appli
31	330	15.0	461	11	US-11-260-192-2	Sequence 2, Appli
32	302.5	13.8	655	8	US-10-505-928-843	Sequence 843, App
33	302.5	13.8	655	8	US-10-196-749-418	Sequence 418, App
34	302.5	13.8	655	9	US-10-194-487-418	Sequence 418, App
35	302.5	13.8	655	9	US-10-195-883-418	Sequence 418, App
36	302.5	13.8	655	9	US-10-195-888-418	Sequence 418, App
37	302.5	13.8	655	9	US-10-195-889-418	Sequence 418, App
38	302.5	13.8	655	9	US-10-216-161A-64	Sequence 64, Appli
39	302.5	13.8	655	11	US-11-072-175-199	Sequence 199, App
40	282.5	12.9	391	11	US-11-105-172-4	Sequence 4, Appli
41	264.5	12.0	229	9	US-10-924-074-8	Sequence 8, Appli
42	264.5	12.0	237	9	US-10-924-074-6	Sequence 6, Appli
43	264.5	12.0	244	9	US-10-924-074-2	Sequence 2, Appli
44	264	12.0	191	9	US-10-924-074-4	Sequence 4, Appli
45	264	12.0	197	10	US-11-211-917-139	Sequence 139, App

ALIGNMENTS

RESULT 1

US-10-510-876-4
; Sequence 4, Application US/10510876
; Publication No. US20060003928A1
; GENERAL INFORMATION:
; APPLICANT: Power, Christine
; APPLICANT: Plater-Zyberk, Christine
; TITLE OF INVENTION: Use of osteoprotegerin for the treatment and/or prevention of fi
; FILE REFERENCE: SLII-P01-001
; CURRENT APPLICATION NUMBER: US/10/510,876
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: EPO2100364.5
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-876-4

Query Match	100.0%	Score	2198	DB	9	Length	401
Best Local Similarity	100.0%	Pred. No.	6.4e-173	Mismatches	0	Indels	0
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QY	61	VCAPCPDHYTDSMHTSDECLYCSVCKELQVVKQECNRNHRVCEKGRYLEIEFCLK	120				
DB	61	VCAPCPDHYTDSMHTSDECLYCSVCKELQVVKQECNRNHRVCEKGRYLEIEFCLK	120				
QY	121	HRSCPPGGVQAGTPERTNVCRCPDGFFSNSTSKAPCRKHTNCSVGLLTQKGNAT	180				
DB	121	HRSCPPGGVQAGTPERTNVCRCPDGFFSNSTSKAPCRKHTNCSVGLLTQKGNAT	180				
QY	181	HDNICSNGSESTQKCGIDVTLCEEAFFFAVPTKFTPNWLSVLDNLPCTKYNASVERI	240				
DB	181	HDNICSNGSESTQKCGIDVTLCEEAFFFAVPTKFTPNWLSVLDNLPCTKYNASVERI	240				
QY	241	KRQHSQBTQQLLKLWKHQKQAQIVKKIQIDILCENSQVORHIGHANLTPEQLRSLME	300				

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Db 241 KROHSSQEQTFOLLKWLKHONKAQDIVKKIIQIDILCENSQVRHGHANLTPQLRSLME 300
Qy 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLGLMHALKHSHKTYHFPKT 360
Db 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLGLMHALKHSHKTYHFPKT 360
Qy 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 2
US-10-510-876-2
; Sequence 2, Application US/10510876
; Publication No. US2006000328A1
; GENERAL INFORMATION:
; APPLICANT: Power, Christine
; TITLE OF INVENTION: Use of osteoprotegerin for the treatment and/or prevention of fib
; TITLE OF INVENTION: disease
; FILE REFERENCE: SLII-P01-801
; CURRENT APPLICATION NUMBER: US/10/510,876
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: EP02100364.5
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-876-2

Query Match 99.7%; Score 2192; DB 9; Length 401;
Best Local Similarity 99.8%; Pred. No. 2e-172;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHQLLDCDCPPGYLKHCHTAKWKT 60
Db 1 MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHQLLDCDCPPGYLKHCHTAKWKT 60
Qy 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLK 120
Db 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLK 120
Qy 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTOKGNAT 180
Db 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTOKGNAT 180
Qy 181 HDNICSGNSESTQKCGIDVTLCCEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERI 240
Db 181 HDNICSGNSESTQKCGIDVTLCCEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERI 240
Qy 241 KROHSSQEQTFOLLKWLKHONKAQDIVKKIIQIDILCENSQVRHGHANLTPQLRSLME 300
Db 241 KROHSSQEQTFOLLKWLKHONKAQDIVKKIIQIDILCENSQVRHGHANLTPQLRSLME 300
Qy 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLGLMHALKHSHKTYHFPKT 360
Db 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLGLMHALKHSHKTYHFPKT 360
Qy 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 3
US-10-921-793-52
; Sequence 52, Application US/10921793
; Publication No. US20060039949A1
; GENERAL INFORMATION:
; APPLICANT: Nycz, Jeffrey
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
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; TITLE OF INVENTION: Osteoinductive Material
; FILE REFERENCE: 64118.000087
; CURRENT APPLICATION NUMBER: US/10/921,793
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-793-52

Query Match 99.7%; Score 2192; DB 9; Length 401;
Best Local Similarity 99.8%; Pred. No. 2e-172;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHQLLDCDCPPGYLKHCHTAKWKT 60
Db 1 MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHQLLDCDCPPGYLKHCHTAKWKT 60
Qy 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLK 120
Db 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLK 120
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Db 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTOKGNAT 180
Qy 181 HDNICSGNSESTQKCGIDVTLCCEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERI 240
Db 181 HDNICSGNSESTQKCGIDVTLCCEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERI 240
Qy 241 KROHSSQEQTFOLLKWLKHONKAQDIVKKIIQIDILCENSQVRHGHANLTPQLRSLME 300
Db 241 KROHSSQEQTFOLLKWLKHONKAQDIVKKIIQIDILCENSQVRHGHANLTPQLRSLME 300
Qy 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLGLMHALKHSHKTYHFPKT 360
Db 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLGLMHALKHSHKTYHFPKT 360
Qy 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 4
US-10-931-198-52
; Sequence 52, Application US/10931198
; Publication No. US20060045902A1
; GENERAL INFORMATION:
; APPLICANT: Nycz, Jeffrey
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
; TITLE OF INVENTION: Osteoinductive Material
; FILE REFERENCE: 64118.000087
; CURRENT APPLICATION NUMBER: US/10/931,198
; CURRENT FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-198-52

Query Match 99.7%; Score 2192; DB 9; Length 401;
Best Local Similarity 99.8%; Pred. No. 2e-172;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHQLLDCDCPPGYLKHCHTAKWKT 60
Db 1 MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHQLLDCDCPPGYLKHCHTAKWKT 60
Qy 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLK 120
Db 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLK 120
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 19:19:25 ; Search time 92 Seconds
(without alignments)
1821.191 Million cell updates/sec

Title: US-09-718-725A-125
Perfect score: 2198
Sequence: 1 MNKLCCALVFLDISIKWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2198	100.0	401	4	US-10-151-071-8 Sequence 8, Appli
3	2198	100.0	401	4	US-10-467-243-2 Sequence 2, Appli
4	2198	100.0	401	5	US-10-129-595-3 Sequence 3, Appli
5	2198	100.0	401	5	US-10-966-845-4 Sequence 4, Appli
6	2198	100.0	401	5	US-10-762-159-125 Sequence 125, App
7	2194	99.8	401	6	US-11-058-073-125 Sequence 125, App
8	2193	99.8	400	4	US-10-142-658-2 Sequence 2, Appli
9	2192	99.7	401	4	US-10-066-209-1 Sequence 1, Appli
10	2192	99.7	401	4	US-10-105-934-2 Sequence 2, Appli
11	2192	99.7	401	4	US-10-164-592-2 Sequence 3, Appli
12	2192	99.7	401	4	US-10-044-674-3 Sequence 2, Appli
13	2192	99.7	401	4	US-10-322-673-5 Sequence 5, Appli
14	2192	99.7	401	4	US-10-139-785-5 Sequence 5, Appli
15	2192	99.7	401	5	US-10-895-676-2 Sequence 2, Appli
16	2192	99.7	401	5	US-10-986-046-5 Sequence 5, Appli
17	2192	99.7	401	5	US-10-986-047-5 Sequence 5, Appli
18	2192	99.7	401	5	US-10-966-845-2 Sequence 2, Appli
19	2192	99.7	401	5	US-10-775-204-528 Sequence 528, App
20	2192	99.7	401	5	US-10-775-204-529 Sequence 529, App
21	2192	99.7	401	5	US-10-775-204-542 Sequence 542, App
22	2192	99.7	401	5	US-10-775-204-1238 Sequence 1238, App
23	2192	99.7	401	5	US-10-775-204-1239 Sequence 1239, App
24	2192	99.7	401	5	US-10-775-204-1240 Sequence 1240, App
25	2192	99.7	401	5	US-10-775-204-1241 Sequence 1241, App
26	2192	99.7	401	5	US-10-775-204-1242 Sequence 1242, App
27	2192	99.7	401	5	US-10-775-204-1243 Sequence 1243, App

28	2192	99.7	401	5	US-10-775-204-1244	Sequence 1244, Ap
29	2192	99.7	401	5	US-10-775-204-1245	Sequence 1245, Ap
30	2192	99.7	401	5	US-10-981-465-5	Sequence 5, Appli
31	2192	99.7	401	5	US-10-981-621-5	Sequence 5, Appli
32	2192	99.7	401	5	US-10-981-673-5	Sequence 5, Appli
33	2192	99.7	401	5	US-10-981-691-5	Sequence 5, Appli
34	2192	99.7	401	5	US-10-986-349-5	Sequence 5, Appli
35	2192	99.7	401	5	US-10-986-376-5	Sequence 5, Appli
36	2192	99.7	986	5	US-10-775-204-312	Sequence 312, App
37	2192	99.7	986	5	US-10-775-204-326	Sequence 326, App
38	2187	99.5	401	3	US-09-062-113-5	Sequence 5, Appli
39	2187	99.5	401	4	US-10-183-091-1	Sequence 1, Appli
40	2187	99.5	401	4	US-10-364-045-1	Sequence 1, Appli
41	2187	99.5	401	4	US-10-232-858-5	Sequence 5, Appli
42	2187	99.5	401	4	US-10-377-076-1	Sequence 1, Appli
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45	2187	99.5	401	5	US-10-929-958-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-405-032-125
; Sequence 125, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 24-Sep-1999
; APPLICATION NUMBER: US/09/405,032
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-09-405-032-125

Query Match 100.0%; Score 2198; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-175;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNKLCCALVFLDISIKWTTQETPPKYLHYDEETSHQLCDKCPGTYLKHCHTAKWKT	60
Db	1	MNKLCCALVFLDISIKWTTQETPPKYLHYDEETSHQLCDKCPGTYLKHCHTAKWKT	60
QY	61	VCAPCPDHYTDSWHTSDECLYCSVCKELQVVKQECNTHNRVCEKGRVLEIEFCLK	120
Db	61	VCAPCPDHYTDSWHTSDECLYCSVCKELQVVKQECNTHNRVCEKGRVLEIEFCLK	120
QY	121	HRSCPPGFGVQAGTPERTVCKPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT	180

Db 121 HRSPPGFGVVQAGTPERTNTVKRCPDGFSSKAPCRKHTNCSVFGLLLTQKGNAT 180
Qy 181 HDNCSGNSESTQKCGIDVTLCCEAFAFFPAVPTKFTPNWLSVLDNLPCTKVNAESVERI 240
Db 181 HDNCSGNSESTQKCGIDVTLCCEAFAFFPAVPTKFTPNWLSVLDNLPCTKVNAESVERI 240
Qy 241 KRQSSQEQTFQLLKLWKHQKQAQDIVKKIQQIDIDLCNSVQRHIGHANLTFEQLRSLME 300
Db 241 KRQSSQEQTFQLLKLWKHQKQAQDIVKKIQQIDIDLCNSVQRHIGHANLTFEQLRSLME 300
Qy 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRINKGQDQTLKGLMHALKHSKTYHPFKT 360
Db 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRINKGQDQTLKGLMHALKHSKTYHPFKT 360
Qy 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401
Db 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401

RESULT 2

US-10-151-071-8
; Sequence 8, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William
; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-071-8

Query Match 100.0%; Score 2198; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-175;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNKLLCCALVFLDISIKWTTQETPPKYLHYDEETSHQLLDCDCKPCTYKHOCTAKWKT 60
Db 1 MNKLLCCALVFLDISIKWTTQETPPKYLHYDEETSHQLLDCDCKPCTYKHOCTAKWKT 60
Qy 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
Db 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
Qy 121 HRSPPGFGVVQAGTPERTNTVKRCPDGFSSKAPCRKHTNCSVFGLLLTQKGNAT 180
Db 121 HRSPPGFGVVQAGTPERTNTVKRCPDGFSSKAPCRKHTNCSVFGLLLTQKGNAT 180
Qy 181 HDNCSGNSESTQKCGIDVTLCCEAFAFFPAVPTKFTPNWLSVLDNLPCTKVNAESVERI 240
Db 181 HDNCSGNSESTQKCGIDVTLCCEAFAFFPAVPTKFTPNWLSVLDNLPCTKVNAESVERI 240
Qy 241 KRQSSQEQTFQLLKLWKHQKQAQDIVKKIQQIDIDLCNSVQRHIGHANLTFEQLRSLME 300
Db 241 KRQSSQEQTFQLLKLWKHQKQAQDIVKKIQQIDIDLCNSVQRHIGHANLTFEQLRSLME 300
Qy 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRINKGQDQTLKGLMHALKHSKTYHPFKT 360
Db 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRINKGQDQTLKGLMHALKHSKTYHPFKT 360
Qy 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401
Db 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401

RESULT 3
US-10-467-243-2
; Sequence 2, Application US/10467243
; Publication No. US20040132971A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Holdings Ltd.
; APPLICANT: Haaning, Jesper Mortensen
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
; FILE REFERENCE: 0226w0310
; CURRENT APPLICATION NUMBER: US/10/467,243
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: DK PA 2001 00214
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00498
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/278,320
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-467-243-2

Query Match 100.0%; Score 2198; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-175;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNKLLCCALVFLDISIKWTTQETPPKYLHYDEETSHQLLDCDCKPCTYKHOCTAKWKT 60
Db 1 MNKLLCCALVFLDISIKWTTQETPPKYLHYDEETSHQLLDCDCKPCTYKHOCTAKWKT 60
Qy 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
Db 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
Qy 121 HRSPPGFGVVQAGTPERTNTVKRCPDGFSSKAPCRKHTNCSVFGLLLTQKGNAT 180
Db 121 HRSPPGFGVVQAGTPERTNTVKRCPDGFSSKAPCRKHTNCSVFGLLLTQKGNAT 180
Qy 181 HDNCSGNSESTQKCGIDVTLCCEAFAFFPAVPTKFTPNWLSVLDNLPCTKVNAESVERI 240
Db 181 HDNCSGNSESTQKCGIDVTLCCEAFAFFPAVPTKFTPNWLSVLDNLPCTKVNAESVERI 240
Qy 241 KRQSSQEQTFQLLKLWKHQKQAQDIVKKIQQIDIDLCNSVQRHIGHANLTFEQLRSLME 300
Db 241 KRQSSQEQTFQLLKLWKHQKQAQDIVKKIQQIDIDLCNSVQRHIGHANLTFEQLRSLME 300
Qy 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRINKGQDQTLKGLMHALKHSKTYHPFKT 360
Db 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRINKGQDQTLKGLMHALKHSKTYHPFKT 360
Qy 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401
Db 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401

RESULT 4

US-10-129-595-3
; Sequence 3, Application US/10129595
; Publication No. US20050031583A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc. et al.
; TITLE OF INVENTION: Uses of OPG Ligand to Modulate Immune Responses
; FILE REFERENCE: P1830F1
; CURRENT APPLICATION NUMBER: US/10/129,595
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/278,215
; PRIOR FILING DATE: 2001-03-23

GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 18:59:30 ; Search time 28.3333 Seconds
(without alignments)
1170.104 Million cell updates/sec

Title: US-09-718-725A-125
Perfect score: 2198
Sequence: 1 MNKLLCCALVFLDISIKWT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilea1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2198	100.0	401	2	US-08-974-022-6
2	2198	100.0	401	2	US-09-042-785A-12
3	2198	100.0	401	2	US-08-795-445A-6
4	2198	100.0	401	2	US-08-795-447A-6
5	2198	100.0	401	2	US-08-974-186-6
6	2198	100.0	401	2	US-08-795-446B-6
7	2198	100.0	401	2	US-08-706-945D-128
8	2198	100.0	401	2	US-08-577-788C-6
9	2198	100.0	401	2	US-08-577-788C-56
10	2198	100.0	401	2	US-09-064-832-2
11	2192	99.7	401	2	US-09-153-927-1
12	2192	99.7	401	2	US-09-072-993C-1
13	2187	99.5	401	2	US-10-232-858-5
14	2187	99.5	401	2	US-09-338-063A-5
15	2177	99.0	401	2	US-10-232-858-62
16	2177	99.0	401	2	US-10-232-858-63
17	2177	99.0	401	2	US-10-232-858-64
18	2177	99.0	401	2	US-10-232-858-66
19	2177	99.0	401	2	US-09-338-063A-62
20	2177	99.0	401	2	US-09-338-063A-63
21	2177	99.0	401	2	US-09-338-063A-64
22	2177	99.0	401	2	US-09-338-063A-65
23	2177	99.0	401	2	US-09-338-063A-66
24	2177	99.0	401	2	US-09-338-063A-67
25	2174	98.9	399	2	US-10-232-858-73
26	2174	98.9	399	2	US-09-338-063A-73
27	2141	97.4	393	2	US-10-232-858-79

28	2141	97.4	393	2	US-09-338-063A-79	Sequence 79, Appl
29	2138.5	97.3	394	2	US-10-232-858-9	Sequence 9, Appli
30	2138.5	97.3	394	2	US-09-338-063A-9	Sequence 9, Appli
31	2138	97.3	391	2	US-10-232-858-106	Sequence 106, App
32	2138	97.3	391	2	US-09-338-063A-106	Sequence 106, App
33	2079	94.6	380	2	US-10-232-858-4	Sequence 4, Appli
34	2079	94.6	380	2	US-09-338-063A-4	Sequence 4, Appli
35	1982	90.2	364	2	US-08-706-945D-142	Sequence 142, App
36	1969.5	89.6	362	2	US-10-232-858-11	Sequence 11, Appl
37	1969.5	89.6	362	2	US-09-338-063A-11	Sequence 11, Appl
38	1942	88.4	363	2	US-10-232-858-69	Sequence 69, Appl
39	1942	88.4	363	2	US-09-338-063A-69	Sequence 69, Appl
40	1930	87.8	351	2	US-10-232-858-74	Sequence 74, Appl
41	1930	87.8	351	2	US-09-338-063A-74	Sequence 74, Appl
42	1919	87.3	359	2	US-10-232-858-70	Sequence 70, Appl
43	1919	87.3	359	2	US-09-338-063A-70	Sequence 70, Appl
44	1910.5	86.9	360	2	US-10-232-858-67	Sequence 67, Appl
45	1910.5	86.9	360	2	US-09-338-063A-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-6

Query Match 100.0%; Score 2198; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.7e-196;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNKLLCCALVFLDISIKWTQTTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKT 60
DB 1 MNKLLCCALVFLDISIKWTQTTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKT 60
QY 61 VCAPCPDHYTDSWHTSDCLYCSGVCKELQYVKQECNRTNHRVCECKEGRYLEIFCLIK 120

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Db      61  VCPCPDHYTDSWHTSDECLYCSVCKELQYVKQECNRTNHRVCECKEGRYLETEFCCLK 120
QY      121  HRSCEPGGVQAGTPTERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
Db      121  HRSCEPGGVQAGTPTERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY      181  HDNCSGSESTQKCGIDVTLCCEAFPRFAVPTKTPNWLVDNLTPTKVNESVERI 240
Db      181  HDNCSGSESTQKCGIDVTLCCEAFPRFAVPTKTPNWLVDNLTPTKVNESVERI 240
QY      241  KRQSSQEQTFQLLKWKHONKAQDIKKIIQDIDLCENSVORHIGHANLTPEQLRSLME 300
Db      241  KRQSSQEQTFQLLKWKHONKAQDIKKIIQDIDLCENSVORHIGHANLTPEQLRSLME 300
QY      301  SLPGKVGAEDEIKTIKACKPSDQILKLLSLRWIRKNGDQDTLKGLMHALKSHKTYHFPKT 360
Db      301  SLPGKVGAEDEIKTIKACKPSDQILKLLSLRWIRKNGDQDTLKGLMHALKSHKTYHFPKT 360
QY      361  VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401
Db      361  VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

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RESULT 2

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US-09-042-785A-12
; Sequence 12, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-12

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Query Match      100.0%; Score 2198; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.7e-196;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHOLLCDKCPGTYLKQHCTAKWKT 60

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Db      1  MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHOLLCDKCPGTYLKQHCTAKWKT 60
QY      61  VCPCPDHYTDSWHTSDECLYCSVCKELQYVKQECNRTNHRVCECKEGRYLETEFCCLK 120
Db      61  VCPCPDHYTDSWHTSDECLYCSVCKELQYVKQECNRTNHRVCECKEGRYLETEFCCLK 120
QY      121  HRSCEPGGVQAGTPTERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
Db      121  HRSCEPGGVQAGTPTERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY      181  HDNCSGSESTQKCGIDVTLCCEAFPRFAVPTKTPNWLVDNLTPTKVNESVERI 240
Db      181  HDNCSGSESTQKCGIDVTLCCEAFPRFAVPTKTPNWLVDNLTPTKVNESVERI 240
QY      241  KRQSSQEQTFQLLKWKHONKAQDIKKIIQDIDLCENSVORHIGHANLTPEQLRSLME 300
Db      241  KRQSSQEQTFQLLKWKHONKAQDIKKIIQDIDLCENSVORHIGHANLTPEQLRSLME 300
QY      301  SLPGKVGAEDEIKTIKACKPSDQILKLLSLRWIRKNGDQDTLKGLMHALKSHKTYHFPKT 360
Db      301  SLPGKVGAEDEIKTIKACKPSDQILKLLSLRWIRKNGDQDTLKGLMHALKSHKTYHFPKT 360
QY      361  VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401
Db      361  VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

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RESULT 3

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US-08-795-445A-6
; Sequence 6, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-6

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Query Match      100.0%; Score 2198; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.7e-196;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHOLLCDKCPGTYLKQHCTAKWKT 60

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 18:47:04 ; Search time 123.333 Seconds
(without alignments)

2293.920 Million cell updates/sec

Title: US-09-718-725A-125

Perfect score: 2198

Sequence: 1 MNKLCCALVFLDISIKWT.....QKLFLMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2187	99.5	401	2 Q53FX6_HUMAN	Q53FX6 homo sapien
3	1906	86.7	401	1 TR11B_RAT	O08727 rattus norv
4	1906	86.7	401	2 Q6P112_MOUSE	Q6P112 mus musculu
5	1892	86.1	401	1 TR11B_MOUSE	O08712 mus musculu
6	1598.5	72.7	402	2 Q4P9K2_CHICK	Q4P9K2 gallus gall
7	1035.5	47.1	387	2 Q6GLN3_XENLA	Q6GLN3 xenopus lae
8	613	27.9	146	2 Q7ZZY4_CHICK	Q7ZZY4 gallus gall
9	576.5	26.2	480	2 Q4SH87_TETNG	Q4SH87 tetraodon n
10	450	20.5	186	2 Q7ZZY5_CHICK	Q7ZZY5 gallus gall
11	444	20.2	300	1 TNR6B_HUMAN	Q95407 homo sapien
12	411.5	18.7	302	2 Q9PUS0_SALPO	Q9PUS0 salvelinus
13	380.5	17.3	285	2 Q90W71_ONCMY	Q90W71 oncorhynch
14	372.5	16.9	285	2 Q90YS6_ONCMY	Q90YS6 oncorhynch
15	365	16.6	286	2 Q6NW61_BRARE	Q6NW61 brachydanio
16	346	15.7	561	2 Q4SH86_TETNG	Q4SH86 tetraodon n
17	345	15.7	637	2 Q5TYN2_BRARE	Q5TYN2 brachydanio
18	344	15.7	474	1 TNR1B_MOUSE	Q5TYN2 brachydanio
19	344	15.7	474	2 Q545P4_MOUSE	Q545P4 mus musculu
20	343	15.6	459	2 Q62327_MOUSE	Q62327 mus musculu
21	333	15.2	461	2 Q6VAU8_RAT	Q6VAU8 rattus norv
22	333	15.2	474	1 TNR1B_RAT	Q80WY6 rattus norv
23	333	15.2	474	2 Q5YLP0_RAT	Q5YLP0 rattus norv
24	330	15.0	461	1 TNR1B_HUMAN	P20333 h tumor nec
25	330	15.0	461	2 Q5THJ6_HUMAN	Q5THJ6 homo sapien
26	329	15.0	651	2 Q98SM6_CHICK	Q98SM6 gallus gall
27	322.5	14.7	433	2 Q91ZM6_RAT	Q91ZM6 rattus norv
28	302.5	13.8	655	1 TNR21_HUMAN	Q75509 homo sapien
29	298	13.6	483	2 Q800K7_PAROL	Q800K7 paralichthy
30	297	13.5	457	2 Q81VSC_HUMAN	Q81VSC homo sapien
31	294	13.4	655	1 TNR21_MOUSE	Q98PUS mus musculu

32	294	13.4	655	2 Q543Y9_MOUSE	Q543Y9 mus musculu
33	285	13.0	289	2 Q4QW2_RAT	Q4QW2 rattus norv
34	284.5	12.9	289	1 TNR5_MOUSE	P27512 mus musculu
35	284.5	12.9	289	2 Q542B1_MOUSE	Q542B1 mus musculu
36	284.5	12.9	289	2 Q8K2X6_MOUSE	Q8K2X6 mus musculu
37	279.5	12.7	467	2 Q800I0_CHICK	Q800I0 gallus gall
38	274.5	12.5	321	2 Q59EP9_HUMAN	Q59EP9 homo sapien
39	270	12.3	169	2 Q9JKE0_RAT	Q9JKE0 rattus norv
40	269.5	12.3	625	1 TNR11_MOUSE	Q5305 mus musculu
41	268	12.2	462	2 Q805B0_CHICK	Q805B0 gallus gall
42	268	12.2	462	2 Q5ZL08_CHICK	Q5ZL08 gallus gall
43	268	12.2	463	2 Q4RF28_TETNG	Q4RF28 tetraodon n
44	267.5	12.2	616	1 TNR11_HUMAN	Q9Y6G6 homo sapien
45	267	12.1	278	2 Q8SQ34_PIG	Q8SQ34 sus scrofa

ALIGNMENTS

RESULT 1
ID TR11B_HUMAN STANDARD; PRT; 401 AA.
AC O00300; Q60236; Q9UHP4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN Name=TNFRSF11B; Synonyms=OCIF, OPG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung cancer;
RA MEDLINE=98151033; PubMed=9492069; DOI=10.1210/en.139.3.1329;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE, AND VARIANT ASN-3.
RC TISSUE=Placenta;
RA MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ASN-3 AND MET-104.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leitchauer B.J., Nickerson D.A.;
RT "NIHNS-SNPs, environmental genome project, NIHNS ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";

RL Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ASN-3.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP PROTEIN SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=9823845; PubMed=9571159; DOI=10.1006/bbrc.1998.8443;
RA Tomoyasu A., Goto M., Fujie N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.,
RT "Signal peptide prediction based on analysis of experimentally
verified cleavage sites.";
RL Protein Sci. 13:2819-2824 (2004).
RN [8]
RP NUCLEOTIDE SEQUENCE OF 22-393.
RC TISSUE=Placenta;
RX PubMed=12110935;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.,
RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL Acta Biochim. Biophys. Sin. 31:680-684 (1999).
RN [9]
RP PROTEIN SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977; DOI=10.1006/bbrc.1997.6603;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.,
RT "Isolation of a novel cytokine from human fibroblasts that
specifically inhibits osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 234:137-142 (1997).
RN [10]
RP TRAIL BINDING
RX MEDLINE=98269100; PubMed=9603945; DOI=10.1074/jbc.273.23.14363;
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dadds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.,
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL J. Biol. Chem. 273:14363-14367 (1998).
RN [11]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964; DOI=10.1074/jbc.273.9.5117;
RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.,
RT "Characterization of structural domains of human osteoclastogenesis
inhibitory factor.";
RL J. Biol. Chem. 273:5117-5123 (1998).
RN [12]
RP REVIEW.

RX MEDLINE=21395914; PubMed=11505389;
RX DOI=10.1002/1097-0142(20010801)92:3<460::AID-CNCR1344>3.0.CO;2-D;
RA Hofbauer L.C., Neubauer A., Heufelder A.E.,
RT "Receptor activator of nuclear factor-kappaB ligand and
osteoprotegerin: potential implications for the pathogenesis and
treatment of malignant bone diseases.";
RL Cancer 92:460-470 (2001).
RN [13]
RP VARIANT JPD ASP-182 DEL
RX MEDLINE=22176628; PubMed=12189164; DOI=10.1093/hmg/11.18.2119;
RA Cundy T., Hegde M., Naot D., Chong B., King A., Wallace R., Mulley J.,
RA Love D.R., Seidel J., Fawcett M., Banovic T., Callon K.E., Grey A.B.,
RA Reid I.R., Middleton-Hardie C.A., Cornish J.,
RT "A mutation in the gene TNFRSF11B encoding osteoprotegerin causes an
idiopathic hyperphosphatasia phenotype.";
RL Hum. Mol. Genet. 11:2119-2127 (2002).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
its function in osteoclastogenesis. Inhibits the activation of
osteoclasts and promotes osteoclast apoptosis in vitro. Bone
homeostasis seems to depend on the local RANKL/OPG ratio. May also
play a role in preventing arterial calcification. May act as decoy
receptor for TRAIL and protect against apoptosis. TRAIL binding
blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
lymph node, trachea, adrenal gland, testis, and bone marrow.
CC Detected at very low levels in brain, placenta and skeletal
muscle. Highly expressed in fetal kidney, liver and lung.
CC -!- INDUCTION: Up-regulated by increasing calcium-concentration in the
medium and estrogens. Down-regulated by glucocorticoids.
CC -!- PTM: N-glycosylated. Contains sialic acid residues.
CC -!- DISEASE: Defects in TNFRSF11B are the cause of juvenile Paget
disease (JPD) [MIM:239000]; also called hyperostosis or chronic
deformans juvenilis or hereditary hyperphosphatasia or chronic
congenital idiopathic hyperphosphatasia. JPD is a rare autosomal
recessive osteopathy that presents in infancy or early childhood.
The disorder is characterized by rapidly remodeling woven bone,
osteopenia, debilitating fractures, and deformities due to a
markedly accelerated rate of bone remodeling throughout the
skeleton. Approximately 40 cases of JPD have been reported
worldwide. Unless it is treated with drugs that block osteoclast-
mediated skeletal resorption, the disease can be fatal.
CC -!- SIMILARITY: Contains 2 death domains.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

DR EMBL; U94332; AA853709.1; -; mRNA.
DR EMBL; AB002146; BAA25910.1; -; mRNA.
DR EMBL; AB008822; BAA32076.1; -; Genomic DNA.
DR EMBL; AY466112; AAR23265.1; -; Genomic DNA.
DR EMBL; BC030155; AAH30155.1; -; mRNA.
DR EMBL; AF134187; AAF20168.1; -; mRNA.
DR HSSP; O14763; 1D0G.
DR Ensembl; ENSG00000164761; Homo sapiens.
DR HGNC; HGNC:11909; TNFRSF11B.
DR H-InvDB; HIX0007748; -.
DR MIM; 602643; -.
DR MIM; 239000; -.
DR GO; GO:0005576; C:extracellular region; TAS.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.

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OM protein - protein search, using sw model

Run on: May 15, 2006, 18:53:14 ; Search time 21 Seconds
(without alignments)
1837.282 Million cell updates/sec

Title: US-09-718-725A-125
Perfect score: 2198
Sequence: 1 MNKLCCALVFLDISIKWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	344	15.7	474	2 B38634	tumor necrosis fac
2	343	15.6	459	2 I48854	gene murine tumour
3	330	15.0	461	1 A35356	tumor necrosis fac
4	329	15.0	651	2 JC7705	death receptor-6 -
5	284.5	12.9	305	2 A46476	B cell-associated
6	264	12.0	277	2 A60771	B-cell activation
7	239.5	10.9	435	2 I54182	tumor necrosis fac
8	237	10.8	348	2 T28623	hypothetical prote
9	232.5	10.6	349	2 T36858	gene G4R protein -
10	229.5	10.4	349	2 D72175	G2R protein - vari
11	225	10.2	325	2 B43692	T2 protein - myxom
12	219	10.0	326	1 GQVZM1	T2 protein - myxom
13	189.5	8.6	425	1 A26431	nerve growth facto
14	188.5	8.6	314	2 I37383	FAS soluble protei
15	188.5	8.6	427	1 GQHUN	nerve growth facto
16	188	8.6	256	2 B32393	T-cell antigen 4-1
17	186	8.5	335	2 A40036	apoptosis-mediati
18	185	8.4	461	1 GQRTT1	tumor necrosis fac
19	177.5	8.1	416	1 JN0006	nerve growth facto
20	177	8.1	255	2 I38426	lymphocyte activat
21	176	8.0	454	1 GQMT1	tumor necrosis fac
22	174	7.9	277	2 I37552	OX40 homolog - hum
23	172	7.8	271	2 S12783	OX40 antigen precu
24	168	7.6	455	1 GQHUT1	tumor necrosis fac
25	168	7.6	461	2 JC4302	tumor necrosis fac
26	158	7.2	595	2 A42086	CD30 antigen precu
27	152.5	6.9	272	2 I48700	gene ox40 protein
28	152	6.9	324	2 JC2395	Fas antigen precu
29	140	6.4	327	2 A46484	apoptosis-mediati

30 139 6.3 1548 2 S34583 serine proteinase
31 138.5 6.3 643 2 T25473 hypothetical prote
32 135.5 6.2 2823 2 F87908 protein T22A3.8 [i
33 135.5 6.2 2823 2 T23064 hypothetical prote
34 135.5 6.2 3102 2 T43291 laminin alpha chai
35 134 6.1 598 2 T33383 hypothetical prote
36 133 6.1 1252 2 S36016 oocyst wall protei
37 132.5 6.0 1786 1 MMHUB1 laminin beta-1 cha
38 130 5.9 1790 1 MMFFB1 laminin beta-1 cha
39 129.5 5.9 1369 2 S70713 protein-tyrosine k
40 129.5 5.9 2918 2 A54105 fibrillin-2 precur
41 128.5 5.8 899 2 G02428 subillin-like pr
42 128.5 5.8 915 2 JC6148 subillin-like pr
43 128 5.8 3712 2 S18253 laminin alpha-1 ch
44 127.5 5.8 2610 2 T20968 hypothetical prote
45 126.5 5.8 1786 1 MMMSB1 laminin beta-1 cha

ALIGNMENTS

RESULT 1

B38634 tumor necrosis factor receptor type 2 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: B38634; A40254; S54816

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A>Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor

A:Reference number: A38634; MUID:91187885; PMID:1849278

A:Accession: B38634

A:Molecule type: mRNA

A:Residues: 1-474 <LEW>

A:Cross-references: UNIPROT:P25119; UNIPARC:UPI0000003E93; GB:M60469; NID:G199827; PIDN

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen.

Mol. Cell. Biol. 11, 3020-3026, 1991

A>Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A:Reference number: A40254; MUID:91246168; PMID:1645445

A:Accession: A40254

A:Molecule type: mRNA

A:Residues: 1-474 <GOO>

A:Cross-references: UNIPARC:UPI0000003B93; GB:M60469; NID:G199827; PIDN:AAA39752.1; PID

R:Kisnerghis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.

submitted to the EMBL Data Library, May 1995

A:Description: Characterization of the promoter region of the murine p75-TNF receptor.

A:Reference number: S54816

A:Accession: S54816

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-22 <KIS>

A:Cross-references: UNIPARC:UPI000016CF95; EMBL:X87128; NID:G809043; PIDN:CAA60618.1; P

C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homol.

C:Keywords: cytokine receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>

F:40-77/Domain: NGF receptor repeat homology <NG1>

F:79-120/Domain: NGF receptor repeat homology <NG2>

F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 15.7%; Score 344; DB 2; Length 474;

Best Local Similarity 33.3%; Pred. No. 4.8e-16;

Matches 83; Conservative 28; Mismatches 94; Indels 44; Gaps 9;

OY 5 LCCALVFLDISIKWTTQTTFPPKYL-----HYDEETSHQLLCKCPG 47

DB 6 LWALVLP-ELQL-WATGHTVPAQVLLTPYKPPGYECQISQVEYDRKA--QMCCAKCPG 61

OY 48 TYLQKHCTAKWKTVCAPCDPHYITDSWHTSDECLYCSVPCKELQVVKQECNTHNRVCSC 107

DB 62 QYVHFCKNTSDTVCADCEASMYQVWQNFRTCLSCSSCTTDDVEIRACTQQRNVAC 121

OY 108 KEGRYLEIEF-----CLKHRSPPGFGVQAGTPERNTVCKRCPDGGFFSNSSKAPC 160

```

: ||| :
122 EAGRYCALKTHSGSCQCRWLSKCGPGGVASSRPNAGNVLCCKACAPGTFSDTTSSTDVC 181
QY 161 RKHTWCVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTLCERAFPRFVPTKFTPNWL 220
: ||| :
182 RPHRICSLAI-----PGNASTDAVCA--PESPTLSAIPRTL-----YVSPQEPSTRSQP--- 228
QY 221 SVLVNDNLPG 229
: ||| :
229 ---LDQEPG 234

RESULT 2
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A:Accession: I48854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: I48854; MUID:95178848; PMID:7873884
A:Accession: I48854
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: UNIPROT:Q62327; UNIPARC:UPI00000E7DE6; EMBL:X76401; NID:G433830; PID
A:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 15.6%; Score 343; DB 2; Length 459;
Best Local Similarity 33.1%; Pred. No. 5.4e-16;
Matches 78; Conservative 25; Mismatches 91; Indels 42; Gaps 7;

QY 18 WTTQTFPPKYL-----HYDEETSHQLLDCDKCPGPGTYLKQHCYAKWKT 60
: ||| :
2 WATCHTPVPAQVVLTPYKPEPGVEYCIQSEIYDRKA--QMCCAKCPGQYVXHFCKNTSDT 59
: ||| :

QY 61 VCAPCPDHYTDSWTSDECLYCSVCKELQVQKQECNRTNVRVCEKGEYLEIF--- 117
: ||| :
60 VCADCEASMTQVWQNFRTCLSCSSCSSTQVETRACTKQQRNVRVACBAGRYCALKTHSG 119
: ||| :

QY 118 ---CLKHSRCPGPGVGVOAGTPERTVCKPCDGFNSNETSSKAPCRKHTNCSVFGLL 173
: ||| :
120 SCRCQWRLSKCGPGGVASSRPNAGNVLCCKACAPGTFSDTTSSTDVCPRHCISLAI-- 177
: ||| :

QY 174 TQKGNATHDNICSGNSESTQKCGIDVTLCERAFPRFVPTKFTPNWLSVLVDNLPG 229
: ||| :
178 --PGNASTDAVCA--PESPTLSAIPRTL-----YVSPQEPSTRSQP-----LDQEPG 219
: ||| :

RESULT 3
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A:Reference number: A35356; MUID:90260639; PMID:2160731
A:Accession: A35356
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SMI>
A:Cross-references: UNIPROT:P20333; UNIPARC:UPI000002FAB1; GB:M32315; NID:g189185; PIDN:
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A:Reference number: A36475; MUID:91045991; PMID:2172983
A:Accession: A36475
A:Status: preliminary
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A:Molecule type: mRNA
A:Residues: 1-195,'R',197-461 <KOH>
A:Cross-references: UNIPARC:UPI0000003475F; GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36
R:Dembic, Z.; Loeschner, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A:Reference number: A48416; MUID:91370690; PMID:1966549
A:Accession: A48416
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 23-461 <DEM>
A:Cross-references: UNIPARC:UPI00001736E6; GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:
A>Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A:Reference number: A36007; MUID:90349572; PMID:2166946
A:Accession: A36007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 118-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A:Cross-references: UNIPARC:UPI000016B4D8; GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:
R:Loeschner, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A:Reference number: A23666; MUID:91056048; PMID:2173696
A:Accession: A23666
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-40;65-69;136-141;300-306 <LOE>
A:Cross-references: UNIPARC:UPI000002D39D; UNIPARC:UPI00001736E7; UNIPARC:UPI00001736B8;
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: B35010
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
A:Cross-references: UNIPARC:UPI00001736EA
R:Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
A:Reference number: I38094; MUID:95121934; PMID:7821811
A:Accession: I38094
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: UNIPARC:UPI00000006D8; EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PI
C:Genetics:
A:Gene: GDB:TNFR2
A:Cross-references: GDB:I25914; OMIM:191191
A:Map position: 1p36.2-1p36.2
A:Introns: 26/3
A>Note: the list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-279/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.0%; Score 330; DB 1; Length 461;
Best Local Similarity 39.8%; Pred. No. 4.1e-15;
Matches 66; Conservative 16; Mismatches 77; Indels 12; Gaps 3;

QY 30 HYDEETSHQLLDCDKCPGPGTYLKQHCYAKWKTVCAPCPDHYTDSWTSDECLYCSVCKE 89
: ||| :
: ||| :
: ||| :
```

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 18:46:34 ; Search time 115.667 Seconds
(without alignments)
1523.264 Million cell updates/sec

Title: US-09-718-725A-125
Perfect score: 2198
Sequence: 1 MNKLCCALVFLDISIKWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2198	100.0	401	2 AAW38345	AAW38345 Human ost
2	2198	100.0	401	3 AAY43400	Aay43400 Osteoprot
3	2198	100.0	401	4 AAB66976	Aab66976 Human OPG
4	2198	100.0	401	5 ABG71823	Abg71823 Wild type
5	2198	100.0	401	6 ABP55109	Abp55109 Human ost
6	2198	100.0	401	6 AAE34363	Aae34363 Human ost
7	2198	100.0	401	7 ADD01627	Add01627 Human ost
8	2198	100.0	401	8 ADM28813	Adm28813 Human ost
9	2194	99.8	401	9 AEB19808	Aeb19808 Osteoprot
10	2193	99.8	400	6 ABU08820	Abu08820 Human ost
11	2193	99.8	401	5 ABG73895	Abg73895 Human OPG
12	2193	99.8	401	5 ABG73894	Abg73894 Human OPG
13	2192	99.7	401	2 AAY05742	Aay05742 Tumour ne
14	2192	99.7	401	2 AAW95030	Aaw95030 Tumour ne
15	2192	99.7	401	2 AAW83926	Aaw83926 Human PTH
16	2192	99.7	401	3 AAB18715	Aab18715 A human t
17	2192	99.7	401	4 AAB60570	Aab60570 Human TNF
18	2192	99.7	401	5 ABG73893	Abg73893 Human OPG
19	2192	99.7	401	6 AAE36245	Aae36245 Human TRA
20	2192	99.7	401	6 AAO31135	Aao31135 Human TRA
21	2192	99.7	401	7 ADD01625	Add01625 Human ost
22	2192	99.7	401	7 ADP01625	Adp01625 Human ost
23	2192	99.7	401	7 ADF16158	Adf16158 Human alb
24	2192	99.7	401	7 ADF16153	Adf16153 Human alb
24	2192	99.7	401	7 ADF16151	Adf16151 Human alb

ALIGNMENTS

RESULT 1					
AAW38345					
ID	AAW38345	standard; protein; 401 AA.			
XX					
AC	AAW38345;				
XX					
DT	20-APR-1998	(first entry)			
XX					
DE	Human osteoprotegerin.				
XX					
KW	Osteoprotegerin; antibody; diagnosis; affinity purification;				
KW	recombinant production; transgenic animal; treatment; prevention;				
KW	antisense oligonucleotide; probe; detection; screening; human;				
KW	bone disease; osteoporosis; Paget's disease; hypercalcaemia;				
KW	hyperparathyroidism; rheumatoid arthritis; osteomyelitis;				
KW	osteolytic metastasis; periodontal bone loss; bone necrosis; osteopaenia.				
XX					
OS	Homo sapiens.				
XX					
PN	DE19654610-A1.				
XX					
PD	26-JUN-1997.				
XX					
PF	20-DEC-1996;	96DE-01054610.			
XX					
PR	22-DEC-1995;	95US-00577788.			
XX					
XX	03-SEP-1996;	96US-00706945.			
XX					
PA	(AMGE-) AMGEN INC.				
XX					
PI	Boyle WJ, Lacey DL, Calzone FJ, Chang M;				
XX					
DR	WPI; 1997-334271/31.				
XX					
DR	N-PSDB; AAT96063.				
XX					
PT	Nucleic acid encoding osteoprotegerin - useful for treatment of diseases				
XX	involving excessive bone loss, e.g. osteoporosis.				
XX					
PS	Claim 23; Page 109-111; 182pp; German.				
XX					
CC	The present sequence is human osteoprotegerin (OPG). Anti-OPG antibodies				
XX	can be used in OPG diagnostic assays, and as affinity purification				
CC	materials. The OPG cDNA can be used to express recombinant OPG and to				
CC	generate transgenic animals. It can also be used to regulate the level of				
CC	OPG in mammals, specifically to increase OPG levels, however the use of				
CC	antisense sequences is also contemplated. Fragments of the cDNA can be				
CC	used as probes to detect OPG expressing cells and tissue, and to screen				

Adf15231 Human alb
Adf16152 Human alb
Adf16154 Human alb
Adf16155 Human alb
Adf16156 Human alb
Adf15230 Human alb
Adf15244 Human alb
Adf16157 Human alb
Adk82154 Human TRA
Ady34172 Human TRA
Aea27537 Human TRI
Aea55153 Human TRA
Aeb19868 Human ost
Adf15016 Human alb
Adf15030 Human alb
Abg73890 Human OPG
Abg73891 Human OPG
Aar99925 Full leng
Aaw53239 Human OCI
Aay88622 Osteoclas
Abp70997 Human ost

25 2192 99.7 401 7 ADF15231
26 2192 99.7 401 7 ADF16152
27 2192 99.7 401 7 ADF16154
28 2192 99.7 401 7 ADF16155
29 2192 99.7 401 7 ADF16156
30 2192 99.7 401 7 ADF15230
31 2192 99.7 401 7 ADF15244
32 2192 99.7 401 7 ADF16157
33 2192 99.7 401 8 ADK82154
34 2192 99.7 401 9 ADY34172
35 2192 99.7 401 9 AEA27537
36 2192 99.7 401 9 AEA55153
37 2192 99.7 401 9 AEB19868
38 2192 99.7 986 7 ADF15016
39 2192 99.7 986 7 ADF15030
40 2190 99.6 401 5 ABG73890
41 2188 99.5 401 5 ABG73891
42 2187 99.5 401 2 AAR99925
43 2187 99.5 401 2 AAW53239
44 2187 99.5 401 3 AAY88622
45 2187 99.5 401 6 ABP70997

CC cDNA libraries for related sequences. OPG can be used to treat or prevent
 CC bone diseases, specifically excessive bone loss, e.g. osteoporosis,
 CC Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid
 CC arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,
 CC bone necrosis and osteopaenia
 XX

SQ Sequence 401 AA;

Query Match 100.0%; Score 2198; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.3e-161;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHQLLDCPKPPGYLKHCHCTAKWKT 60
 QY 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
 QY 121 HRSPPGFGVVQAGTPERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
 DB 121 HRSPPGFGVVQAGTPERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
 QY 181 HDNICSGNSESTQKCGIDVTLCEAFAFFAVPTKFTPNWLSVLDNLPGTKVNAESVERI 240
 DB 181 HDNICSGNSESTQKCGIDVTLCEAFAFFAVPTKFTPNWLSVLDNLPGTKVNAESVERI 240
 QY 241 KRQSSSQBOTFQLLWKHQKAQDIVKKIIQDIDLCSNSVQRHIGHANLTFEQLRSLME 300
 DB 241 KRQSSSQBOTFQLLWKHQKAQDIVKKIIQDIDLCSNSVQRHIGHANLTFEQLRSLME 300
 QY 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSWRIKNGDQDTLKGIMHALKHSKTYHFPKT 360
 DB 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSWRIKNGDQDTLKGIMHALKHSKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401

RESULT 2

AA43400
 ID AAY43400 standard; protein; 401 AA.
 XX
 AC AAY43400;
 XX
 DT 28-JAN-2000 (first entry)
 XX
 DE Osteoprotegerin protein sequence.
 XX
 KW Osteoprotegerin; OPG; human; cardiovascular disease; occlusion;
 KW calcification; blood vessel; atherosclerosis; medial calcific sclerosis;
 KW Monckeberg's arteriosclerosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO9953942-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 21-APR-1999; 99WO-US008793.
 XX
 PR 23-APR-1998; 98US-00064832.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Simonet S, Sarosi I;
 XX
 DR WPI: 2000-013182/01.
 DR N-PSDB; AA237254.
 XX
 PT Treating and preventing cardiovascular diseases, especially

PT atherosclerosis and Monckeberg's arteriosclerosis.

XX Claim 9; Page 37-39; 43pp; English.

XX This sequence represents the human osteoprotegerin (OPG). The invention relates to a method of treating or preventing cardiovascular disease by administering OPG. The method can be used to treat and prevent cardiovascular diseases associated with occlusion and calcification of blood vessels, especially atherosclerosis or Monckeberg's arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or prevent cardiovascular diseases provides an alternative to invasive treatments. OPG can be used as a single therapeutic for prevention and treatment of both osteoporosis and cardiovascular diseases

SQ Sequence 401 AA;

Query Match 100.0%; Score 2198; DB 3; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.3e-161;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MNKLLCCALVFLDISIKWTTQETPPPKYLHYDEETSHQLLDCPKPPGYLKHCHCTAKWKT 60
 QY 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
 QY 121 HRSPPGFGVVQAGTPERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
 DB 121 HRSPPGFGVVQAGTPERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
 QY 181 HDNICSGNSESTQKCGIDVTLCEAFAFFAVPTKFTPNWLSVLDNLPGTKVNAESVERI 240
 DB 181 HDNICSGNSESTQKCGIDVTLCEAFAFFAVPTKFTPNWLSVLDNLPGTKVNAESVERI 240
 QY 241 KRQSSSQBOTFQLLWKHQKAQDIVKKIIQDIDLCSNSVQRHIGHANLTFEQLRSLME 300
 DB 241 KRQSSSQBOTFQLLWKHQKAQDIVKKIIQDIDLCSNSVQRHIGHANLTFEQLRSLME 300
 QY 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSWRIKNGDQDTLKGIMHALKHSKTYHFPKT 360
 DB 301 SLPGKKVGAEDIEKTIKACKPSDQILKLLSWRIKNGDQDTLKGIMHALKHSKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNQVQSVKISCL 401

RESULT 3

AA66976
 ID AAB66976 standard; protein; 401 AA.
 XX
 AC AAB66976;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Human OPG.
 XX
 KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
 KW ischaemia; Parkinson's disease.
 XX
 OS Homo sapiens.
 XX
 FN WO2000103719-A2.
 XX
 PT 18-JAN-2001.
 XX

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 19:21:20 ; Search time 16 Seconds
(without alignments)
1176.655 Million cell updates/sec

Title: US-09-718-725A-123
Perfect score: 2179
Sequence: 1 MNKWLCCALLVLLDIIETWT.....QKLFLFMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
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2: /SID85/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SID85/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SID85/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SID85/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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9: /SID85/ptodata/1/pubpaa/US10_NEW_PUB.pep1.*
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12: /SID85/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2179	100.0	401	9 US-10-948-053-2	Sequence 2, Appli
2	1900	87.2	401	9 US-10-510-876-2	Sequence 2, Appli
3	1900	87.2	401	9 US-10-921-793-52	Sequence 52, Appl
4	1900	87.2	401	9 US-10-931-198-52	Sequence 52, Appl
5	1900	87.2	401	9 US-10-942-042-52	Sequence 52, Appl
6	1895	87.0	401	11 US-11-231-963-1	Sequence 1, Appli
7	1895	87.0	401	11 US-11-254-836-1	Sequence 1, Appli
8	1892	86.8	401	9 US-10-510-876-4	Sequence 4, Appli
9	1821	83.6	537	11 US-11-144-236-6	Sequence 6, Appli
10	1820	83.5	380	11 US-11-144-236-1	Sequence 1, Appli
11	1629	74.8	338	9 US-10-921-793-54	Sequence 54, Appl
12	1629	74.8	338	9 US-10-931-198-54	Sequence 54, Appl
13	1629	74.8	338	9 US-10-942-042-54	Sequence 54, Appl
14	922.5	42.3	406	9 US-10-948-053-6	Sequence 6, Appli
15	898	41.2	407	9 US-10-948-053-3	Sequence 3, Appli
16	893.5	41.0	400	9 US-10-948-053-4	Sequence 4, Appli
17	893.5	41.0	400	9 US-10-948-053-5	Sequence 5, Appli
18	892	40.9	404	9 US-10-948-053-7	Sequence 7, Appli
19	888	40.8	401	9 US-10-948-053-8	Sequence 8, Appli
20	838	38.5	161	11 US-11-154-257-3	Sequence 3, Appli
21	615	28.2	120	11 US-11-042-814-8	Sequence 8, Appli

22	424.5	19.5	300	11	US-11-154-257-2	Sequence 2, Appli
23	314	14.4	461	11	US-11-132-285-6	Sequence 6, Appli
24	314	14.4	461	11	US-11-182-946-4	Sequence 4, Appli
25	312	14.3	461	8	US-10-511-937-2945	Sequence 2945, Ap
26	312	14.3	461	9	US-10-523-328-5	Sequence 5, Appli
27	312	14.3	461	10	US-11-183-218-32	Sequence 32, Appl
28	312	14.3	461	11	US-11-183-205-32	Sequence 32, Appl
29	312	14.3	461	11	US-11-260-192-2	Sequence 2, Appli
30	312	14.3	474	11	US-11-260-192-4	Sequence 4, Appli
31	301.5	13.8	655	8	US-10-505-928-843	Sequence 843, App
32	301.5	13.8	655	8	US-10-196-749-418	Sequence 418, App
33	301.5	13.8	655	9	US-10-194-487-418	Sequence 418, App
34	301.5	13.8	655	9	US-10-195-883-418	Sequence 418, App
35	301.5	13.8	655	9	US-10-195-888-418	Sequence 418, App
36	301.5	13.8	655	9	US-10-195-889-418	Sequence 418, App
37	301.5	13.8	655	9	US-10-216-161A-64	Sequence 64, Appl
38	301.5	13.8	655	11	US-11-072-175-199	Sequence 199, App
39	300	13.8	235	11	US-11-126-126-16	Sequence 16, Appl
40	265.5	12.2	391	11	US-11-105-172-4	Sequence 4, Appli
41	261	12.0	191	9	US-10-924-074-4	Sequence 139, App
42	261	12.0	197	10	US-11-211-917-139	Sequence 8, Appli
43	261	12.0	229	9	US-10-924-074-8	Sequence 6, Appli
44	261	12.0	237	9	US-10-924-074-6	Sequence 2, Appli
45	261	12.0	244	9	US-10-924-074-2	

ALIGNMENTS

RESULT 1

US-10-948-053-2

; Sequence 2, Application US/10948053

; Publication No. US20060019887A1

; GENERAL INFORMATION:

; APPLICANT: Dunstan, Colin R.

; TITLE OF INVENTION: Compositions and Methods for the Prevention or Treatment of Cancer

; FILE OF INVENTION: Bone Loss Associated with Cancer

; FILE REFERENCE: A-605

; CURRENT APPLICATION NUMBER: US/10/948,053

; CURRENT FILING DATE: 2004-09-22

; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/389,545

; PRIOR FILING DATE: CURRENT FILING DATE: 1999-09-03

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 401

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-948-053-2

Query Match	100.0%;	Score 2179;	DB 9;	Length 401;
Best Local Similarity	100.0%;	Pred. No. 1.8e-167;		
Matches 401;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MNKLCCALLVLLDIIETWTQTLPKYLHYDPETGHQLLCDKCAPGTLYLKQHCTVRRKT	60	
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Db	61	LCVPCPDHSYTDTSWTSDECVYCSVCKELQSVQECNTHNRVCECEGRYLEIFCLK	120	
QY	121	HRSCPPGSGVQAGTPERNVCKCPDGFPSGETSSKAPCIKHTWCSTGLLLIOKGNAT	180	
Db	121	HRSCPPGSGVQAGTPERNVCKCPDGFPSGETSSKAPCIKHTWCSTGLLLIOKGNAT	180	
QY	181	HDNCSGNREATQKCGIDVTLCCEAFRFAVPTKIIPNWLSDLPGTKVNAESVERI	240	
Db	181	HDNCSGNREATQKCGIDVTLCCEAFRFAVPTKIIPNWLSDLPGTKVNAESVERI	240	
QY	241	KRRHSSQQTQQLLKLWKHQRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLALME	300	
Db	241	KRRHSSQQTQQLLKLWKHQRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLALME	300	

	Qy	301	SIPGKKISPEEIERTRKTKCKSEQLLKLLSWRINKGDQDTLKGIMYALKHLKLTSHPPKT	360
	Db	301	SIPGKKISPEEIERTRKTKCKSEQLLKLLSWRINKGDQDTLKGIMYALKHLKLTSHPPKT	360
	Qy	361	VTHSLRKTNRFLLHSFTMYRLYOKLFLEMIGNQVQSIVKISCL	401
	Db	361	VTHSLRKTNRFLLHSFTMYRLYOKLFLEMIGNQVQSIVKISCL	401

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 19:19:25 ; Search time 92 Seconds
(without alignments)
1821.191 Million cell updates/sec

Title: US-09-718-725A-123
Perfect score: 2179
Sequence: 1 MNKWLCCALLVLLDIIEWTT.....QKLFLFMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2179	100.0	401	3	US-09-389-782-2
2	2179	100.0	401	3	US-09-405-032-123
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4	2164	99.3	401	6	US-11-058-073-123
5	2079	95.4	401	3	US-09-405-032-121
6	2079	95.4	401	5	US-10-762-159-121
7	2071	95.0	401	6	US-11-058-073-121
8	2061	94.6	380	3	US-09-405-032-138
9	2061	94.6	380	5	US-10-762-159-138
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12	1900	87.2	401	4	US-10-105-934-2
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16	1900	87.2	401	4	US-10-139-785-5
17	1900	87.2	401	5	US-10-895-676-2
18	1900	87.2	401	5	US-10-986-046-5
19	1900	87.2	401	5	US-10-986-047-5
20	1900	87.2	401	5	US-10-966-845-2
21	1900	87.2	401	5	US-10-775-204-528
22	1900	87.2	401	5	US-10-775-204-529
23	1900	87.2	401	5	US-10-775-204-542
24	1900	87.2	401	5	US-10-775-204-1238
25	1900	87.2	401	5	US-10-775-204-1239
26	1900	87.2	401	5	US-10-775-204-1240
27	1900	87.2	401	5	US-10-775-204-1241

28	1900	87.2	401	5	US-10-775-204-1242	Sequence 1242, Ap
29	1900	87.2	401	5	US-10-775-204-1243	Sequence 1243, Ap
30	1900	87.2	401	5	US-10-775-204-1244	Sequence 1244, Ap
31	1900	87.2	401	5	US-10-775-204-1245	Sequence 1245, Ap
32	1900	87.2	401	5	US-10-981-465-5	Sequence 5, Appli
33	1900	87.2	401	5	US-10-981-621-5	Sequence 5, Appli
34	1900	87.2	401	5	US-10-981-673-5	Sequence 5, Appli
35	1900	87.2	401	5	US-10-981-691-5	Sequence 5, Appli
36	1900	87.2	401	5	US-10-986-349-5	Sequence 5, Appli
37	1900	87.2	401	5	US-10-986-376-5	Sequence 5, Appli
38	1900	87.2	986	5	US-10-775-204-312	Sequence 312, App
39	1900	87.2	986	5	US-10-775-204-326	Sequence 326, App
40	1895	87.0	401	3	US-09-062-113-5	Sequence 5, Appli
41	1895	87.0	401	4	US-10-183-091-1	Sequence 1, Appli
42	1895	87.0	401	4	US-10-364-045-1	Sequence 1, Appli
43	1895	87.0	401	4	US-10-232-858-5	Sequence 5, Appli
44	1895	87.0	401	4	US-10-377-076-1	Sequence 1, Appli
45	1895	87.0	401	4	US-10-785-109-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-389-782-2
; Sequence 2, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-2

Query Match	100.0%;	Score 2179;	DB 3;	Length 401;
Best Local Similarity	100.0%;	Pred. No. 4.4e-171;		
Matches	401;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MNKLCCALLVLLDIIEWTTQTLPPKYLHYDPETGHLCCDKCAPGTYLKHCTVRRKT	60	
Db	1	MNKLCCALLVLLDIIEWTTQTLPPKYLHYDPETGHLCCDKCAPGTYLKHCTVRRKT	60	
Qy	61	LCVPCPDHSYTDWSHTSDECVYCVCKELQSVKQECNRTHNRVCECEGRVLEIEFCLK	120	
Db	61	LCVPCPDHSYTDWSHTSDECVYCVCKELQSVKQECNRTHNRVCECEGRVLEIEFCLK	120	
Qy	121	HRSCPPGSGVQAGTPPERTVCKCPDGFSSKAPCIKHTNCSTFGLLIQKGNAT	180	
Db	121	HRSCPPGSGVQAGTPPERTVCKCPDGFSSKAPCIKHTNCSTFGLLIQKGNAT	180	
Qy	181	HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLPGTKVNAESVERI	240	
Db	181	HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLPGTKVNAESVERI	240	
Qy	241	KRRHSSQOTQLLWKHQRDQEMVKIIQDIDLCSSVQRHGHNSLTTEQLLALME	300	
Db	241	KRRHSSQOTQLLWKHQRDQEMVKIIQDIDLCSSVQRHGHNSLTTEQLLALME	300	
Qy	301	SLPGKKISPEIERTRKTCKSEQLLKLSLWRIKNGQDQTLKGLMYALKHLKTSHPFKT	360	
Db	301	SLPGKKISPEIERTRKTCKSEQLLKLSLWRIKNGQDQTLKGLMYALKHLKTSHPFKT	360	
Qy	361	VTHSLRKTMRFLHSTMYRLYOKLFLEMIGNOVQSVKISCL	401	
Db	361	VTHSLRKTMRFLHSTMYRLYOKLFLEMIGNOVQSVKISCL	401	

Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 2

US-09-405-032-123

/ Sequence 123, Application US/09405032

/ Publication No. US20030207827A1

/ GENERAL INFORMATION:

/ APPLICANT: Amgen Inc.

/ TITLE OF INVENTION: OSTEOPROTEGERIN

/ NUMBER OF SEQUENCES: 168

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Amgen Inc.

/ STREET: 1840 Dehavilland Drive

/ CITY: Thousand Oaks

/ STATE: California

/ COUNTRY: United States

/ ZIP: 91320

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/405,032

/ FILING DATE: 24-Sep-1999

/ CLASSIFICATION: <unknown>

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Winter, Robert B.

/ REFERENCE/DOCKET NUMBER: A-378-CIP2

/ INFORMATION FOR SEQ ID NO: 123:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 401 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

/ SEQUENCE DESCRIPTION: SEQ ID NO: 123:

US-09-405-032-123

Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 4.4e-171;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIIEWTQTETLPKYLHYDPETGHQLLCKDCAPGTVLKQHCIVRRKT 60
Db 1 MNKWLCCALLVLLDIIIEWTQTETLPKYLHYDPETGHQLLCKDCAPGTVLKQHCIVRRKT 60
QY 61 LCVPCPDHSYTDSDWHTSDVCVYSPVKELQSVKQECNTHNRVCECEBGRYLEIEFCILK 120
Db 61 LCVPCPDHSYTDSDWHTSDVCVYSPVKELQSVKQECNTHNRVCECEBGRYLEIEFCILK 120
QY 121 HRSCTPPGSGVQAGTPERTNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSCTPPGSGVQAGTPERTNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
QY 181 HDNVCNGNEATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLVDSLPGTKVNASVERI 240
Db 181 HDNVCNGNEATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLVDSLPGTKVNASVERI 240
QY 241 KRHSSEQEOTFOLLKWLKHQRDQEMVKII IQDIDLCESSVQRHLGSHSLTTTEQLLALME 300
Db 241 KRHSSEQEOTFOLLKWLKHQRDQEMVKII IQDIDLCESSVQRHLGSHSLTTTEQLLALME 300
QY 301 SLPGKKISPEEIERTRKTKSSEQLLKLSLRWIRKNGDQDTLKGMLYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEEIERTRKTKSSEQLLKLSLRWIRKNGDQDTLKGMLYALKHLKTSHPFKT 360

QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 3

US-10-762-159-123

/ Sequence 123, Application US/10762159

/ Publication No. US20050221331A1

/ GENERAL INFORMATION:

/ APPLICANT: Boyle, William J.

/ APPLICANT: Lacey, David L.

/ APPLICANT: Calzone, Frank J.

/ APPLICANT: Chang, Ming-Shi

/ TITLE OF INVENTION: OSTEOPROTEGERIN

/ NUMBER OF SEQUENCES: 168

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Amgen Inc.

/ STREET: 1840 Dehavilland Drive

/ CITY: Thousand Oaks

/ STATE: California

/ COUNTRY: United States

/ ZIP: 91320

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/10/762,159

/ FILING DATE: 2004-JAN-20

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/09/132,985

/ FILING DATE: 1998-AUG-12

/ APPLICATION NUMBER: 08/771,777

/ FILING DATE:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Winter, Robert B.

/ REFERENCE/DOCKET NUMBER: A-378-CIP

/ INFORMATION FOR SEQ ID NO: 123:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 401 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

US-10-762-159-123

Query Match 100.0%; Score 2179; DB 5; Length 401;
Best Local Similarity 100.0%; Pred. No. 4.4e-171;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIIEWTQTETLPKYLHYDPETGHQLLCKDCAPGTVLKQHCIVRRKT 60
Db 1 MNKWLCCALLVLLDIIIEWTQTETLPKYLHYDPETGHQLLCKDCAPGTVLKQHCIVRRKT 60
QY 61 LCVPCPDHSYTDSDWHTSDVCVYSPVKELQSVKQECNTHNRVCECEBGRYLEIEFCILK 120
Db 61 LCVPCPDHSYTDSDWHTSDVCVYSPVKELQSVKQECNTHNRVCECEBGRYLEIEFCILK 120
QY 121 HRSCTPPGSGVQAGTPERTNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSCTPPGSGVQAGTPERTNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
QY 181 HDNVCNGNEATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLVDSLPGTKVNASVERI 240
Db 181 HDNVCNGNEATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLVDSLPGTKVNASVERI 240
QY 241 KRHSSEQEOTFOLLKWLKHQRDQEMVKII IQDIDLCESSVQRHLGSHSLTTTEQLLALME 300
Db 241 KRHSSEQEOTFOLLKWLKHQRDQEMVKII IQDIDLCESSVQRHLGSHSLTTTEQLLALME 300
QY 301 SLPGKKISPEEIERTRKTKSSEQLLKLSLRWIRKNGDQDTLKGMLYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEEIERTRKTKSSEQLLKLSLRWIRKNGDQDTLKGMLYALKHLKTSHPFKT 360

QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: May 15, 2006, 18:59:30 ; Search time 28.3333 Seconds
(without alignments)
1170.104 Million cell updates/sec
Title: US-09-718-725A-123
Perfect score: 2179
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Total number of hits satisfying chosen parameters: 572060
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2179	100.0	401	2	US-08-974-022-4
2	2179	100.0	401	2	US-09-042-785A-13
3	2179	100.0	401	2	US-08-795-445A-4
4	2179	100.0	401	2	US-08-795-447A-4
5	2179	100.0	401	2	US-08-974-186-4
6	2179	100.0	401	2	US-08-795-446B-4
7	2179	100.0	401	2	US-08-706-945D-126
8	2179	100.0	401	2	US-08-577-788C-4
9	2179	100.0	401	2	US-08-577-788C-54
10	2079	95.4	401	2	US-08-974-022-2
11	2079	95.4	401	2	US-08-795-445A-2
12	2079	95.4	401	2	US-08-795-447A-2
13	2079	95.4	401	2	US-08-974-186-2
14	2079	95.4	401	2	US-08-795-446B-2
15	2079	95.4	401	2	US-08-706-945D-124
16	2079	95.4	401	2	US-08-577-788C-2
17	2079	95.4	401	2	US-08-577-788C-55
18	1955	89.7	364	2	US-08-706-945D-141
19	1900	87.2	401	2	US-09-153-927-1
20	1900	87.2	401	2	US-09-072-993C-1
21	1895	87.0	401	2	US-10-232-858-5
22	1895	87.0	401	2	US-09-338-063A-5
23	1892	86.8	401	2	US-08-974-022-6
24	1892	86.8	401	2	US-09-042-785A-12
25	1892	86.8	401	2	US-08-795-445A-6
26	1892	86.8	401	2	US-08-795-447A-6
27	1892	86.8	401	2	US-08-974-186-6

28	1892	86.8	401	2	US-08-795-446B-6	Sequence 6, Appli
29	1892	86.8	401	2	US-08-706-945D-128	Sequence 128, App
30	1892	86.8	401	2	US-08-577-788C-6	Sequence 6, Appli
31	1892	86.8	401	2	US-08-577-788C-56	Sequence 56, Appl
32	1892	86.8	401	2	US-09-064-832-2	Sequence 2, Appli
33	1885	86.5	401	2	US-10-232-858-62	Sequence 62, Appl
34	1885	86.5	401	2	US-10-232-858-63	Sequence 63, Appl
35	1885	86.5	401	2	US-10-232-858-64	Sequence 64, Appl
36	1885	86.5	401	2	US-10-232-858-65	Sequence 65, Appl
37	1885	86.5	401	2	US-10-232-858-66	Sequence 66, Appl
38	1885	86.5	401	2	US-09-338-063A-62	Sequence 62, Appl
39	1885	86.5	401	2	US-09-338-063A-63	Sequence 63, Appl
40	1885	86.5	401	2	US-09-338-063A-64	Sequence 64, Appl
41	1885	86.5	401	2	US-09-338-063A-65	Sequence 65, Appl
42	1885	86.5	401	2	US-09-338-063A-66	Sequence 66, Appl
43	1882	86.4	399	2	US-10-232-858-73	Sequence 73, Appl
44	1882	86.4	399	2	US-09-338-063A-73	Sequence 73, Appl
45	1862.5	85.5	391	2	US-10-232-858-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-08-974-022-4
; Sequence 4, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-4

Query Match	100.0%;	Score 2179;	DB 2;	Length 401;
Best Local Similarity	100.0%;	Pred. No. 3.4e-195;		
Matches 401;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MNKLCCALLVLLDIIEWTTQETLPKYLHYDPETGHOLLCDCAPGTYLKQHCTVRRKT	60	
QY	61	LCVPCPDHSYTDMSHTSDCVYCSVPKELQSVKQECNRNHRVCEEGRYLEIFCLK	120	

Db 61 LCVPCPDHSDYSDSHSDECVYCSVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSCEPGSGVQAGTPERTNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSCEPGSGVQAGTPERTNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
QY 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVSLPOTKVNASSVERI 240
Db 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVSLPOTKVNASSVERI 240
QY 241 KRHSSEQOTFOLLKWKHONRDQEMVKIIQDIDLCSSVQRHLGHSNLTTEQLLALME 300
Db 241 KRHSSEQOTFOLLKWKHONRDQEMVKIIQDIDLCSSVQRHLGHSNLTTEQLLALME 300
QY 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 2

US-09-042-785A-13
; Sequence 13, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-09-042-785A-13

Query Match 100.0%; Score 2179; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.4e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIETWTOETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60
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Db 1 MNKWLCCALLVLLDIIETWTOETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60
QY 61 LCVPCPDHSDYSDSHSDECVYCSVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCPDHSDYSDSHSDECVYCSVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSCEPGSGVQAGTPERTNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSCEPGSGVQAGTPERTNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
QY 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVSLPOTKVNASSVERI 240
Db 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVSLPOTKVNASSVERI 240
QY 241 KRHSSEQOTFOLLKWKHONRDQEMVKIIQDIDLCSSVQRHLGHSNLTTEQLLALME 300
Db 241 KRHSSEQOTFOLLKWKHONRDQEMVKIIQDIDLCSSVQRHLGHSNLTTEQLLALME 300
QY 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 3

US-08-795-445A-4
; Sequence 4, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-4

Query Match 100.0%; Score 2179; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.4e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIETWTOETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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(without alignments)
2293.920 Million cell updates/sec

Title: US-09-718-725A-123

Perfect score: 2179

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Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2159	99.1	401	2 Q6P112_MOUSE	Q6P112 mus musculus
3	2079	95.4	401	1 TR11B_RAT	O08727 rattus norv
4	1900	87.2	401	1 TR11B_HUMAN	O00300 homo sapien
5	1895	87.0	401	2 Q53FX6_HUMAN	Q53FX6 homo sapien
6	1484.5	68.1	402	2 Q4F9K2_CHICK	Q4F9K2 gallus gall
7	1014	46.5	387	2 Q6GLN3_XENLA	Q6GLN3 xenopus lae
8	553	25.4	480	2 Q4SH87_TETNG	Q4SH87 tetraodon n
9	541	24.8	146	2 Q7ZZY4_CHICK	Q7ZZY4 gallus gall
10	428	19.6	186	2 Q7ZZY5_CHICK	Q7ZZY5 gallus gall
11	424.5	19.5	300	1 TNR6B_HUMAN	O95407 homo sapien
12	397.5	18.2	286	2 Q6NW61_BRARE	Q6NW61 brachydanio
13	390.5	17.9	302	2 Q9PU50_SALPO	Q9PU50 salvelinus
14	390	17.9	285	2 Q90W71_ONCMY	Q90W71 oncorhynch
15	383	17.6	285	2 Q90YS6_ONCMY	Q90YS6 oncorhynch
16	346.5	15.9	637	2 Q5TYN2_BRARE	Q5TYN2 brachydanio
17	324	14.9	561	2 Q4SH86_TETNG	Q4SH86 tetraodon n
18	314	14.4	459	2 Q62327_MOUSE	Q62327 mus musculus
19	312	14.3	461	1 TNR1B_HUMAN	P20333 h tumor nec
20	312	14.3	461	2 Q5THJ6_HUMAN	Q5THJ6 homo sapien
21	312	14.3	474	1 TNR1B_MOUSE	P25119 mus musculus
22	312	14.3	474	2 Q545P4_MOUSE	Q545P4 m adult mal
23	301.5	13.8	655	1 TNR21_HUMAN	O75509 homo sapien
24	301	13.8	461	2 Q6VAU8_RAT	Q6VAU8 rattus norv
25	301	13.8	474	1 TNR1B_RAT	O80WY6 rattus norv
26	301	13.8	474	2 Q5YLP0_RAT	Q5YLP0 rattus norv
27	300.5	13.8	651	2 Q98SM6_CHICK	Q98SM6 gallus gall
28	288	13.2	655	1 TNR21_MOUSE	Q98PUS mus musculus
29	288	13.2	655	2 Q543Y9_MOUSE	Q543Y9 mus musculus
30	281	12.9	433	2 Q91ZM6_RAT	Q91ZM6 rattus norv
31	275.5	12.6	463	2 Q4RF28_TETNG	Q4RF28 tetraodon n

32	270	12.4	289	1	TNR5_MOUSE	P27512 mus musculus
33	270	12.4	289	2	Q542B1_MOUSE	Q542B1 mus musculus
34	270	12.4	289	2	Q8K2X6_MOUSE	Q8K2X6 mus musculus
35	268.5	12.3	467	2	Q80010_CHICK	Q80010 gallus gall
36	268.5	12.3	625	1	TNR11_MOUSE	Q35305 mus musculus
37	268	12.3	289	2	Q4QQW2_RAT	Q4QQW2 rattus norv
38	266.5	12.2	616	1	TNR11_HUMAN	Q9Y6Q6 homo sapien
39	266	12.2	462	2	Q805B0_CHICK	Q805B0 gallus gall
40	266	12.2	462	2	Q5ZL08_CHICK	Q5ZL08 gallus gall
41	263	12.1	457	2	Q81VS6_HUMAN	Q81VS6 homo sapien
42	263	12.1	483	2	Q800K7_PAROL	Q800K7 parolichny
43	261	12.0	223	2	Q86YK5_HUMAN	Q86YK5 homo sapien
44	261	12.0	277	1	TNR5_HUMAN	P25942 homo sapien
45	261	12.0	277	2	Q5U007_HUMAN	Q5U007 homo sapien

ALIGNMENTS

RESULT 1
TR11B_MOUSE
ID TR11B_MOUSE STANDARD; PRT; 401 AA.
AC -O08712; Q70202;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN Name=Thrsf1b; Synonyms=Ocif, Opg;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density."
RL Cell 89:309-319(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
AND ARG-296.
RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RX MEDLINE=98382527; PubMed=9714833; DOI=10.1016/S0378-1119(98)00295-9;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
gene and its expression in embryogenesis."
RL Gene 215:339-343(1998).
RN [3]
RP FUNCTION.
RC MEDLINE=21060987; PubMed=10952716; DOI=10.1084/jem.192.4.463;
RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
Simonet W.S.;
RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
osteoclasts and prevents vascular calcification by blocking a process
resembling osteoclastogenesis."
RL J. Exp. Med. 192:463-474(2000).
RN [4]
RP FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
its function in osteoclastogenesis. Inhibits the activation of
osteoclasts and promotes osteoclast apoptosis in vitro. Bone
homeostasis seems to depend on the local RANKL/OPG ratio. May also
play a role in preventing arterial calcification. May act as decoy
receptor for TRAIL and protect against apoptosis. TRAIL binding

blocks the inhibition of osteoclastogenesis.

-!- SUBUNIT: Homodimer.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta, and in embryo.

-!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7, whereas expression decreases at day 11 and increases from day 15 to 17. On day 15 found in developing bone primordia, brachiocephalic artery and ductus arteriosus, left main bronchus, abdominal aorta and midgut.

-!- INDUCTION: Up-regulated by TGF-beta and estrogens. Down-regulated by 1,25-dihydroxyvitamin D3 and parathyroid hormone.

-!- SIMILARITY: Contains 2 death domains.

-!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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EMBL; U94331; AAB53708.1; -; mRNA.

EMBL; AB013898; BAA28269.1; -; mRNA.

EMBL; AB013903; BAA33388.1; -; Genomic DNA.

HSP; O14763; ID03.

Ensembl; ENSMUSG0000063727; Mus musculus.

MGI; MGI:109587; Tnfrsf1b.

GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IDA.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0042489; P:negative regulation of odontogenesis (sensu. . .; IDA.

InterPro; IPR000488; Death.

InterPro; IPR011029; DEATH-like.

InterPro; IPR001368; TNFR_c6.

Pfam; PF00531; Death; 1.

Pfam; PF00020; TNFR_c6; 3.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 4.

PROSITE; PS50017; DEATH_DOMAIN; 1.

PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS50050; TNFR_NGFR_2; 2.

Apoptosis; Glycoprotein; Polymorphism; Receptor; Repeat; Signal.

SIGNAL 1 21

CHAIN 22 401

By similarity.

Tumor necrosis factor receptor superfamily member 11b.

TNFR-Cys 1.

TNFR-Cys 2.

TNFR-Cys 3.

TNFR-Cys 4.

Death 1.

Death 2.

Involved in dimerization (By similarity).

N-linked (GlcNac. . .) (Potential).

N-linked (GlcNac. . .) (Potential).

N-linked (GlcNac. . .) (Potential).

N-linked (GlcNac. . .) (Potential).

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

R -> P (in strain 129/Ola and strain NIH Swiss).

I -> R (in strain 129/Ola and strain NIH Swiss).

N -> D (in strain 129/Ola and strain NIH Swiss).

S -> A (in strain 129/Ola and strain NIH Swiss).

FT VARIANT 296 296 L -> R (in strain 129/Ola and strain NIH Swiss).

SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 100.0%; Score 2179; DB 1; Length 401;

Best Local Similarity 100.0%; Pred. No. 1.6e-142;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLLDIIEWTTQETLPPKYLHYDVPETGHQLCDKCAPGYLKHQCHVRRKT 60

Db 1 MNKWLCCALLVLLDIIEWTTQETLPPKYLHYDVPETGHQLCDKCAPGYLKHQCHVRRKT 60

Qy 61 LCVPCPDHSYDTSWHTSDECVYCPVKCKELQSVKQECNRTNRVCECEGRYLEIEFCLK 120

Db 61 LCVPCPDHSYDTSWHTSDECVYCPVKCKELQSVKQECNRTNRVCECEGRYLEIEFCLK 120

Qy 121 HRSPCPGSGVVOAGTPERTVCKCPDGFPGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180

Db 121 HRSPCPGSGVVOAGTPERTVCKCPDGFPGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180

Qy 181 HDNVCSGNREATKCGIDVTLCBEAFRFVPTKLIIPNWLVLVDSLPGTKVNAESVERI 240

Db 181 HDNVCSGNREATKCGIDVTLCBEAFRFVPTKLIIPNWLVLVDSLPGTKVNAESVERI 240

Qy 241 KRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300

Db 241 KRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300

Qy 301 SLPGKKSIPBEIERTRTKCKSSEQLLKLWLWRKNGDQDTLKGIMYALKHLKTSHPFKT 360

Db 301 SLPGKKSIPBEIERTRTKCKSSEQLLKLWLWRKNGDQDTLKGIMYALKHLKTSHPFKT 360

Qy 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEIMIGNOVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEIMIGNOVQSVKISCL 401

RESULT 2

Q6P112_MOUSE PRELIMINARY; PRT; 401 AA.

ID Q6P112_MOUSE PRELIMINARY; PRT; 401 AA.

AC Q6P112; 05-JUL-2004 (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE Tumor necrosis factor receptor superfamily, member 11b (Osteoprotegerin).

DE Name=tnfrsf11b;

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX [1]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Limb;

RC MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Sherman C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Morley P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.I., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.J., Skalska U., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.

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OM protein - protein search, using sw model

Run on: May 15, 2006, 18:53:14 ; Search time 21 Seconds
(without alignments)
1837.282 Million cell updates/sec

Title: US-09-718-725A-123
Perfect score: 2179
Sequence: 1 MNKWLCCALLVLDIIIEWTT.....QKLFLFMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	314	14.4	459	2 I48854	gene murine tumour
2	312	14.3	461	1 A35356	tumor necrosis fac
3	312	14.3	474	2 B38634	tumor necrosis fac
4	300.5	13.8	651	2 JC2705	death receptor-6
5	270	12.4	305	2 A46476	B cell-associated
6	261	12.0	277	2 A60771	B-cell activation
7	244	11.2	435	2 I54182	tumor necrosis fac
8	233.5	10.7	325	2 B43692	T2 protein - rabbi
9	220	10.1	326	1 GOVZML	T2 protein - myxom
10	217	10.0	349	2 D36858	Gene G4R protein -
11	216	9.9	349	2 D72175	G2R protein - vari
12	215.5	9.9	348	2 T28623	hypothetical prote
13	199	9.1	427	1 GQHUN	nerve growth facto
14	197.5	9.1	425	1 A26431	nerve growth facto
15	184	8.4	416	1 JN0006	nerve growth facto
16	182	8.4	335	2 A40036	apoptosis-mediated
17	179.5	8.2	314	2 I37383	FAS soluble protein
18	177	8.1	256	2 B32392	T-cell antigen 4-1
19	167	7.7	255	2 I38426	lymphocyte activat
20	165.5	7.6	461	2 JC4302	tumor necrosis fac
21	163	7.5	271	2 S12783	OX40 antigen precu
22	161.5	7.4	454	1 GQWST1	tumor necrosis fac
23	160	7.3	455	1 GQRTU1	tumor necrosis fac
24	153	7.0	461	1 GQRTU1	tumor necrosis fac
25	152.5	7.0	272	2 I48700	gene OX40 protein
26	151	6.9	277	2 I37552	OX40 homolog - hum
27	147.5	6.8	324	2 JC2395	Fas antigen precu
28	143	6.6	327	2 A46484	apoptosis-mediated
29	142.5	6.5	2823	2 F87908	protein T2A3.8 [1

30	142.5	6.5	2823	2 T23064	hypothetical prote
31	142.5	6.5	3102	2 T43291	laminin alpha chai
32	139	6.4	595	2 A42086	CD30 antigen precu
33	137.5	6.3	899	2 G02428	subtilisin-like pr
34	137.5	6.3	915	2 JC6148	subtilisin-like pr
35	133	6.1	1786	1 MMURB1	laminin beta-1 cha
36	131.5	6.0	260	1 A46517	CD27 antigen precu
37	128.5	5.9	1252	2 S36016	oocyst wall protei
38	128.5	5.9	1790	1 MMFFB1	laminin beta-1 cha
39	126.5	5.8	1548	2 S34583	serine proteinase
40	125	5.7	1680	2 A43434	furin (EC 3.4.21.7
41	122	5.6	1372	2 T25933	hypothetical prote
42	120.5	5.5	250	1 A49053	CD27 antigen precu
43	120.5	5.5	2918	2 A54105	fibrillin-2 precu
44	119.5	5.5	1639	1 MMFFB2	laminin gamma-1 ch
45	119	5.5	1364	2 T00250	MEGF2 protein - hu

ALIGNMENTS

RESULT 1

I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48854
R:Powell, E.B.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: I48854; MUID:95178848; PMID:7873884
A:Accession: I48854
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: UNIPROT:Q62327; UNIPARC:UPI00000E7DB6; EMBL:X76401; NID:9433830; PIR:
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homol:
F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 14.4%; Score 314; DB 2; Length 459;
Best Local Similarity 34.6%; Pred. No. 2.6e-14;
Matches 66; Conservative 20; Mismatches 79; Indels 26; Gaps 4;

Qy	18	WTQETLPKYL--HYDEPTGH-----QLCLCDKCAPGYTLKHQCTVRRKTLIC	62
Db	2	WATGHTVPAQVVLTPYKPEPGVECIQSRYDRKAMCCAKCPGGYVKHFCNKTSDTVC	61
Qy	63	VPCPDHSTYDTSWHTSDSCVYCSFVKELQSVKQCNRTNHRVCECEGRYLIIEP----	117
Db	62	ADCEASMTQVMNQFRTCLSCSSCSSTQVETRACTKQQRVCACEAGRYCALKTHSGSC	121
Qy	118	--CLKHSRCPGSGVYVQAGTPERTVCKKCPDPFSGSETSSKAPCIKHTNCSTFGLLLIQ	175
Db	122	RCOMLSKGGPGGVASSRAPNGVNLKACAPGTFTSDTTSVDCRPHRICs-----ILAI	177
Qy	176	KGNATHDNVCS 186	
Db	178	PGNASTDAVCA 188	

RESULT 2

A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; J38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.
Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A:Reference number: A35356; MUID:90260639; PMID:2160731
A:Accession: A35356
A:Status: preliminary

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OM protein - protein search, using sw model

Run on: May 15, 2006, 18:46:34 ; Search time 115.667 Seconds
(without alignments)
1523.264 Million cell updates/sec

Title: US-09-718-725A-123
Perfect score: 2179
Sequence: 1 MNKWLCCALLVLLDLEWT.....QKLFLFMIGNQVSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2179	100.0	401	2 AAW38344	Aaw38344 Mouse ost
2	2179	100.0	401	4 AAB80898	Aab80898 Human ost
3	2179	100.0	401	4 AAY72916	Aay72916 Human ost
4	2179	100.0	401	4 AAB66975	Aab66975 Murine OP
5	2179	100.0	401	8 ADM28811	Adm28811 Mouse ost
6	2179	100.0	401	9 AEB19866	Aebi9866 Murine os
7	2164	99.3	401	9 AEB19806	Aebi9806 Osteoprot
8	2079	95.4	401	2 AAW38343	Aaw38343 Rat osteo
9	2079	95.4	401	4 AAB66974	Aab66974 Rat OP
10	2079	95.4	401	8 ADM28809	Adm28809 Rat osteo
11	2079	95.4	401	9 AEB19867	Aebi9867 Rat osteo
12	2071	95.0	401	9 AEB19804	Aebi9804 Osteoprot
13	2061	94.6	380	4 AAB66987	Aab66987 Human OP
14	2061	94.6	380	8 ADM28826	Adm28826 Mouse ost
15	2061	94.6	380	9 AEB19855	Aebi9855 Osteoprot
16	2050	94.1	380	8 ADM28861	Adm28861 Mouse ost
17	1900	87.2	401	2 AAY05742	Aay05742 Tumour ne
18	1900	87.2	401	2 AAW95030	Aaw95030 Tumour ne
19	1900	87.2	401	2 AAW83926	Aaw83926 Human FTH
20	1900	87.2	401	3 AAB18715	Aabi8715 A human t
21	1900	87.2	401	4 AAB60570	Aab60570 Human TNF
22	1900	87.2	401	6 AAE36245	Aae36245 Human TRF
23	1900	87.2	401	6 AAO31135	Aao31135 Human TRA
24	1900	87.2	401	7 ADD01625	Add01625 Human ost

25	1900	87.2	401	7 ADF16158	Adf16158 Human alb
26	1900	87.2	401	7 ADF16153	Adf16153 Human alb
27	1900	87.2	401	7 ADF16151	Adf16151 Human alb
28	1900	87.2	401	7 ADF15231	Adf15231 Human alb
29	1900	87.2	401	7 ADF16152	Adf16152 Human alb
30	1900	87.2	401	7 ADF16154	Adf16154 Human alb
31	1900	87.2	401	7 ADF16156	Adf16156 Human alb
32	1900	87.2	401	7 ADF16155	Adf16155 Human alb
33	1900	87.2	401	7 ADF15230	Adf15230 Human alb
34	1900	87.2	401	7 ADF15244	Adf15244 Human alb
35	1900	87.2	401	7 ADF16157	Adf16157 Human alb
36	1900	87.2	401	8 ADK82154	Adk82154 Human TRA
37	1900	87.2	401	9 ADY34172	Ady34172 Human TRA
38	1900	87.2	401	9 AEA27537	Aea27537 Human TR1
39	1900	87.2	401	9 AEA55153	Aea55153 Human TR1
40	1900	87.2	401	9 AEB19868	Aebi9868 Human ost
41	1900	87.2	986	7 ADF15016	Adf15016 Human alb
42	1900	87.2	986	7 ADF15030	Adf15030 Human alb
43	1895	87.0	401	2 AAR99925	Aar99925 Full leng
44	1895	87.0	401	2 AAW53239	Aaw53239 Human OCI
45	1895	87.0	401	3 AAY88622	Aay88622 Osteoclas

ALIGNMENTS

RESULT 1
AAW38344
ID AAW38344 standard; protein; 401 AA.
XX
AC AAW38344;
XX
DT 20-APR-1998 (first entry)
XX
DE Mouse osteoprotegerin.
XX
KW Osteoprotegerin; antibody; diagnosis; affinity purification;
KW recombinant production; transgenic animal; treatment; prevention;
KW antisense oligonucleotide; probe; detection; screening; mouse;
KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW osteolytic metastasis; periodontal bone loss; bone necrosis; osteopaenia;
XX murine.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
CDS 90..1295
FT /*tag= a
FT /product= "osteoprotegerin"
DE19654610-A1.
26-JUN-1997.
20-DEC-1996; 96DE-01054610.
22-DEC-1995; 95US-00577788.
03-SEP-1996; 96US-00706945.
(AMGE-) AMGEN INC.
Boyle WJ, Lacey DL, Calzone FJ, Chang M;
WPI; 1997-334271/31.
N-PSDB; AAT96062.
Nucleic acid encoding osteoprotegerin - useful for treatment of diseases involving excessive bone loss, e.g. osteoporosis.
Claim 23; Page 106-107; 182pp; German.
The present sequence is mouse osteoprotegerin (OPG). Anti-OPG antibodies

CC can be used in OPG diagnostic assays, and as affinity purification
 CC materials. The OPG cDNA can be used to express recombinant OPG and to
 CC generate transgenic animals. It can also be used to regulate the level of
 CC OPG in mammals, specifically to increase OPG levels, however the use of
 CC antisense sequences is also contemplated. Fragments of the cDNA can be
 CC used as probes to detect OPG expressing cells and tissue, and to screen
 CC cDNA libraries for related sequences. OPG can be used to treat or prevent
 CC bone diseases, specifically excessive bone loss, e.g. osteoporosis,
 CC Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid
 CC arthritis, osteonvelitis, osteolytic metastases, periodontal bone loss,
 CC bone necrosis and osteopaenia

XX Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.9e-174; Indels 0; Gaps 0;
 Matches 401; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKMLCCALLVLLDIIETWTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60
 DB 1 MNKMLCCALLVLLDIIETWTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60

QY 61 LCVPCPDHSYTDTSWHTSDVCVSPVKELQSVKQECNTRNHRVCEBEGRYLEIEFCLK 120
 DB 61 LCVPCPDHSYTDTSWHTSDVCVSPVKELQSVKQECNTRNHRVCEBEGRYLEIEFCLK 120

QY 121 HRSPPGSGVQAGTPERTNVCKCPDGFSGETSSKAPCIKHTNCSTFGLLIQGNAT 180
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QY 241 KRRHSSQEQTFQLLKLWKHQRNDQEMVKIIQDIDLCESSVQRHLGHSNLTTTEQLLALME 300
 DB 241 KRRHSSQEQTFQLLKLWKHQRNDQEMVKIIQDIDLCESSVQRHLGHSNLTTTEQLLALME 300

QY 301 SLPGKKISPEIERTRKTKCSSEQLLKLWLRIKNGQDITLKGMLYALKHLKTSHPFKT 360
 DB 301 SLPGKKISPEIERTRKTKCSSEQLLKLWLRIKNGQDITLKGMLYALKHLKTSHPFKT 360

QY 361 VTHSLRKTRMFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 DB 361 VTHSLRKTRMFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 2

AAB80898
 ID AAB80898 standard; protein; 401 AA.

AC AAB80898;

DT 31-MAY-2001 (first entry)

DE Human osteoprotegrin, OPG.

KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
 KW osteoclast formation inhibition; bone resorption inhibition.

OS Homo sapiens.

PN WO200117543-A2.

XX 15-MAR-2001.

PF 18-AUG-2000; 2000WO-US022806.

XX 03-SEP-1999; 99US-00389545.

PA (AMGE-) AMGEN INC.

PI Dunstan CR;

XX WPI; 2001-265936/27.

XX Preventing or treating lytic bone diseases, particularly associated with
 PT cancer or metastasis, by administering an osteoprotegrin polypeptide.

XX Claim 5; Fig 2; 87pp; English.

CC The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegrin)
 CC polypeptide or OPG fusion protein (see AAB80899-AAB80904). The present
 CC sequence is human OPG. OPG inhibits formation of osteoclasts (and thus
 CC bone resorption) by blocking differentiation from monocytes/macrophage
 CC precursors. The OPG polypeptide can be used in a method of preventing or
 CC treating lytic bone disease, for preventing metastasis of cancer to bone
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophogeal,
 CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
 CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention
 CC or treatment of loss of bone mass, which occurs in conditions including
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone
 CC metastases

XX Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.9e-174;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 LCVPCPDHSYTDTSWHTSDVCVSPVKELQSVKQECNTRNHRVCEBEGRYLEIEFCLK 120

QY 121 HRSPPGSGVQAGTPERTNVCKCPDGFSGETSSKAPCIKHTNCSTFGLLIQGNAT 180
 DB 121 HRSPPGSGVQAGTPERTNVCKCPDGFSGETSSKAPCIKHTNCSTFGLLIQGNAT 180

QY 181 HDNVCSGNREATKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLDLSLPGTKVNAESVERI 240
 DB 181 HDNVCSGNREATKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLDLSLPGTKVNAESVERI 240

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 DB 241 KRRHSSQEQTFQLLKLWKHQRNDQEMVKIIQDIDLCESSVQRHLGHSNLTTTEQLLALME 300

QY 301 SLPGKKISPEIERTRKTKCSSEQLLKLWLRIKNGQDITLKGMLYALKHLKTSHPFKT 360

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OM protein - protein search, using sw model

Run on: May 15, 2006, 19:21:20 ; Search time 16 Seconds
(without alignments)
1176.655 Million cell updates/sec

Title: US-09-718-725A-121
Perfect score: 2185
Sequence: 1 MNKWLCCALLVFLDIIEWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA-New.*

1: /SID55/ptodata/1/pubpaa/US08_NEW_PUB.pepl.*
2: /SID55/ptodata/1/pubpaa/US06_NEW_PUB.pepl.*
3: /SID55/ptodata/1/pubpaa/US07_NEW_PUB.pepl.*
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6: /SID55/ptodata/1/pubpaa/US03_NEW_PUB.pepl.*
7: /SID55/ptodata/1/pubpaa/US09_NEW_PUB.pepl.*
8: /SID55/ptodata/1/pubpaa/US10_NEW_PUB.pepl.*
9: /SID55/ptodata/1/pubpaa/US10_NEW_PUB.pepl.*
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11: /SID55/ptodata/1/pubpaa/US11_NEW_PUB.pepl.*
12: /SID55/ptodata/1/pubpaa/US60_NEW_PUB.pepl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1914	87.6	401	9 US-10-510-876-2	Sequence 2, Appli
3	1914	87.6	401	9 US-10-921-793-52	Sequence 52, Appl
4	1914	87.6	401	9 US-10-931-198-52	Sequence 52, Appl
5	1914	87.6	401	9 US-10-942-042-52	Sequence 52, Appl
6	1909	87.4	401	11 US-11-231-963-1	Sequence 1, Appli
7	1909	87.4	401	11 US-11-254-836-1	Sequence 1, Appli
8	1906	87.2	401	9 US-10-510-876-4	Sequence 4, Appli
9	1829	83.7	537	11 US-11-144-236-6	Sequence 6, Appli
10	1828	83.7	380	11 US-11-144-236-1	Sequence 1, Appli
11	1639	75.0	338	9 US-10-921-793-54	Sequence 54, Appl
12	1639	75.0	338	9 US-10-931-198-54	Sequence 54, Appl
13	1639	75.0	338	9 US-10-942-042-54	Sequence 54, Appl
14	909	41.6	406	9 US-10-948-053-6	Sequence 6, Appli
15	882	40.4	407	9 US-10-948-053-3	Sequence 3, Appli
16	879	40.2	404	9 US-10-948-053-7	Sequence 7, Appli
17	877	40.1	400	9 US-10-948-053-4	Sequence 4, Appli
18	877	40.1	400	9 US-10-948-053-5	Sequence 5, Appli
19	875	40.0	401	9 US-10-948-053-8	Sequence 8, Appli
20	824	37.7	161	11 US-11-154-257-3	Sequence 3, Appli
21	610	27.9	120	11 US-11-042-814-8	Sequence 8, Appli

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23	322	14.7	461	11	US-11-132-285-6	Sequence 6, Appli
24	322	14.7	461	11	US-11-182-946-4	Sequence 4, Appli
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27	320	14.6	461	9	US-10-523-328-5	Sequence 5, Appli
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29	320	14.6	461	11	US-11-183-205-32	Sequence 32, Appl
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31	314	14.4	235	11	US-11-126-126-16	Sequence 16, Appl
32	304.5	13.9	655	8	US-10-505-928-843	Sequence 843, App
33	304.5	13.9	655	8	US-10-196-749-418	Sequence 418, App
34	304.5	13.9	655	9	US-10-194-487-418	Sequence 418, App
35	304.5	13.9	655	9	US-10-195-883-418	Sequence 418, App
36	304.5	13.9	655	9	US-10-195-888-418	Sequence 418, App
37	304.5	13.9	655	9	US-10-195-889-418	Sequence 418, App
38	304.5	13.9	655	9	US-10-216-161A-64	Sequence 64, Appl
39	304.5	13.9	655	11	US-11-072-175-139	Sequence 199, App
40	271.5	12.4	391	11	US-11-105-172-4	Sequence 4, Appli
41	263	12.0	191	9	US-10-924-074-4	Sequence 4, Appli
42	263	12.0	197	10	US-11-211-917-139	Sequence 139, App
43	263	12.0	229	9	US-10-924-074-8	Sequence 8, Appli
44	263	12.0	237	9	US-10-924-074-6	Sequence 6, Appli
45	263	12.0	244	9	US-10-924-074-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-948-053-2
; Sequence 2, Application US/10948053
; Publication No. US20060019887A1

; GENERAL INFORMATION:
; APPLICANT: Dunstan, Colin R.

; TITLE OF INVENTION: Compositions and Methods for the Prevention or Treatment of Canc

; FILE OF INVENTION: Bone Loss Associated with Cancer

; FILE REFERENCE: A-605

; CURRENT APPLICATION NUMBER: US/10/948,053

; CURRENT FILING DATE: 2004-09-22

; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/389,545

; PRIOR FILING DATE: CURRENT FILING DATE: 1999-09-03

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 401

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-948-053-2

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Best Local Similarity	94.5%	Pred. No. 5.8e-165;	Mismatches 12;	Indels 0;
Matches 379;	Conservative 10;			
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 19:19:25 ; Search time 92 Seconds
(without alignments)
1821.191 Million cell updates/sec

Title: US-09-718-725A-121
Perfect score: 2185
Sequence: 1 MNKWLCCALLVFLDIIEWTT.....QKLFUEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	100.0	401	3	US-09-405-032-121 Sequence 121, App
2	2185	100.0	401	5	US-10-762-159-121 Sequence 121, App
3	2177	99.6	401	6	US-11-058-073-121 Sequence 121, App
4	2079	95.1	401	3	US-09-389-782-2 Sequence 2, Appli
5	2079	95.1	401	3	US-09-405-032-123 Sequence 123, App
6	2079	95.1	401	5	US-10-762-159-123 Sequence 123, App
7	2064	94.5	401	6	US-11-058-073-123 Sequence 123, App
8	1965	89.9	380	3	US-09-405-032-138 Sequence 138, App
9	1965	89.9	380	5	US-10-762-159-138 Sequence 138, App
10	1965	89.9	380	6	US-11-058-073-175 Sequence 175, App
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23	1914	87.6	401	5	US-10-775-204-542 Sequence 542, App
24	1914	87.6	401	5	US-10-775-204-1238 Sequence 1238, Ap
25	1914	87.6	401	5	US-10-775-204-1239 Sequence 1239, Ap
26	1914	87.6	401	5	US-10-775-204-1240 Sequence 1240, Ap
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28	1914	87.6	401	5	US-10-775-204-1242	Sequence 1242, Ap
29	1914	87.6	401	5	US-10-775-204-1243	Sequence 1243, Ap
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ALIGNMENTS

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US-09-405-032-121
; Sequence 121, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESS: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 121:
US-09-405-032-121

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Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 181 HDNVCSGNREATQNGIDVTLCCEAFFRFAVPTKIIIPNWLVSVDLPSTKVNASVERI 240
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Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 2

US-10-762-159-121
; Sequence 121, Application US/10762159
; Publication No. US20050221331A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/762,159
; FILING DATE: 2004-JAN-20
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/132,985
; FILING DATE: 1998-AUG-12
; APPLICATION NUMBER: 08/771,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-762-159-121

Query Match 100.0%; Score 2185; DB 5; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.1e-177; Indels 0; Gaps 0;
Matches 401; Conservative 0; Mismatches 0;
QY 1 MNKWLCCALLVFLDIIIEWTTQETPPPKYLHYDPETGRQLCDKCAPGYLKHQCHTVRRKT 60
Db 1 MNKWLCCALLVFLDIIIEWTTQETPPPKYLHYDPETGRQLCDKCAPGYLKHQCHTVRRKT 60
QY 61 LCVPDPSYSDTSWHTSDECVYCSPVCKELQTVKQECNTRNHRVCEBEGRYLEFCLK 120
Db 61 LCVPDPSYSDTSWHTSDECVYCSPVCKELQTVKQECNTRNHRVCEBEGRYLEFCLK 120

QY 121 HRSPPGLGLVLAQGTPTERTVCKRCPDGFSGSETSSKAPCRKHTNCSSLGILLIIOKGNAT 180
Db 121 HRSPPGLGLVLAQGTPTERTVCKRCPDGFSGSETSSKAPCRKHTNCSSLGILLIIOKGNAT 180
QY 181 HDNVCSGNREATQNGIDVTLCCEAFFRFAVPTKIIIPNWLVSVDLPSTKVNASVERI 240
Db 181 HDNVCSGNREATQNGIDVTLCCEAFFRFAVPTKIIIPNWLVSVDLPSTKVNASVERI 240
QY 241 KRRHSSQEQTFQLLKWKHQRNDQEMVKKIIQDIDLCSSVQRHGHANLTTEQRLILME 300
Db 241 KRRHSSQEQTFQLLKWKHQRNDQEMVKKIIQDIDLCSSVQRHGHANLTTEQRLILME 300
QY 301 SLPGKKISPDIEIRTRKTCSEQLLKLLSLWRIKNGQDITLKGIMYALKHLKAYHFPKT 360
Db 301 SLPGKKISPDIEIRTRKTCSEQLLKLLSLWRIKNGQDITLKGIMYALKHLKAYHFPKT 360
QY 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 3

US-11-058-073-121
; Sequence 121, Application US/11058073
; Publication No. US20050147611A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM J.
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: CALZONE, FRANK J.
; APPLICANT: CHANG, MING-SHI
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS
; FILE REFERENCE: A-378CIPSC
; CURRENT APPLICATION NUMBER: US/11/058,073
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/613,591
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 09/457,647
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 09/350,670
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 08/706,945
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: US 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 121
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Rattus rattus
US-11-058-073-121

Query Match 99.6%; Score 2177; DB 6; Length 401;
Best Local Similarity 99.8%; Pred. No. 5.5e-177;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNKWLCCALLVFLDIIIEWTTQETPPPKYLHYDPETGRQLCDKCAPGYLKHQCHTVRRKT 60
Db 1 MNKWLCCALLVFLDIIIEWTTQETPPPKYLHYDPETGRQLCDKCAPGYLKHQCHTVRRKT 60
QY 61 LCVPDPSYSDTSWHTSDECVYCSPVCKELQTVKQECNTRNHRVCEBEGRYLEFCLK 120
Db 61 LCVPDPSYSDTSWHTSDECVYCSPVCKELQTVKQECNTRNHRVCEBEGRYLEFCLK 120
QY 121 HRSPPGLGLVLAQGTPTERTVCKRCPDGFSGSETSSKAPCRKHTNCSSLGILLIIOKGNAT 180
Db 121 HRSPPGLGLVLAQGTPTERTVCKRCPDGFSGSETSSKAPCRKHTNCSSLGILLIIOKGNAT 180
QY 181 HDNVCSGNREATQNGIDVTLCCEAFFRFAVPTKIIIPNWLVSVDLPSTKVNASVERI 240
Db 181 HDNVCSGNREATQNGIDVTLCCEAFFRFAVPTKIIIPNWLVSVDLPSTKVNASVERI 240

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 18:59:30 ; Search time 28.3333 Seconds
(without alignments)
1170.104 Million cell updates/sec

Title: US-09-718-725A-121
Perfect score: 2185
Sequence: 1 MNKWLCCALLVFLDIIEWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	100.0	401	2	US-08-974-022-2
2	2185	100.0	401	2	US-08-795-445A-2
3	2185	100.0	401	2	US-08-795-447A-2
4	2185	100.0	401	2	US-08-974-186-2
5	2185	100.0	401	2	US-08-795-446B-2
6	2185	100.0	401	2	US-08-706-945D-124
7	2185	100.0	401	2	US-08-577-788C-2
8	2185	100.0	401	2	US-08-577-788C-55
9	2079	95.1	401	2	US-08-974-022-4
10	2079	95.1	401	2	US-09-042-785A-13
11	2079	95.1	401	2	US-08-795-445A-4
12	2079	95.1	401	2	US-08-795-447A-4
13	2079	95.1	401	2	US-08-974-186-4
14	2079	95.1	401	2	US-08-795-446B-4
15	2079	95.1	401	2	US-08-706-945D-126
16	2079	95.1	401	2	US-08-577-788C-4
17	2079	95.1	401	2	US-08-577-788C-54
18	1914	87.6	401	2	US-09-153-927-1
19	1914	87.6	401	2	US-09-072-993C-1
20	1909	87.4	401	2	US-10-232-858-5
21	1909	87.4	401	2	US-09-338-063A-5
22	1906	87.2	401	2	US-08-974-022-6
23	1906	87.2	401	2	US-09-042-785A-12
24	1906	87.2	401	2	US-08-795-445A-6
25	1906	87.2	401	2	US-08-795-447A-6
26	1906	87.2	401	2	US-08-974-186-6
27	1906	87.2	401	2	US-08-795-446B-6

28	1906	87.2	401	2	US-08-706-945D-128
29	1906	87.2	401	2	US-08-577-788C-6
30	1906	87.2	401	2	US-08-577-788C-56
31	1906	87.2	401	2	US-09-064-832-2
32	1899	86.9	401	2	US-10-232-858-62
33	1899	86.9	401	2	US-10-232-858-63
34	1899	86.9	401	2	US-10-232-858-64
35	1899	86.9	401	2	US-10-232-858-65
36	1899	86.9	401	2	US-10-232-858-66
37	1899	86.9	401	2	US-09-338-063A-62
38	1899	86.9	401	2	US-09-338-063A-63
39	1899	86.9	401	2	US-09-338-063A-64
40	1899	86.9	401	2	US-09-338-063A-65
41	1899	86.9	401	2	US-09-338-063A-66
42	1896	86.8	399	2	US-10-232-858-73
43	1896	86.8	399	2	US-09-338-063A-73
44	1876.5	85.9	391	2	US-10-232-858-106
45	1876.5	85.9	391	2	US-09-338-063A-106

ALIGNMENTS

RESULT 1
US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-2

Query Match 100.0%; Score 2185; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.5e-200;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNKWLCCALLVFLDIIEWTTQETPPKYLHYDVPETGROLLCDKCAPGTVLKHQCTVRRKT 60
Db 1 MNKWLCCALLVFLDIIEWTTQETPPKYLHYDVPETGROLLCDKCAPGTVLKHQCTVRRKT 60
QY 61 LCVPCPDYSYDTSWHTSDCVSPCKELQTVKQCNTRNHRVCEBGRYLEFCLK 120

Db 61 LCVPCPDYSDTSWHTSDECVYCSVPCKELQTVKQECNRTNHRVCEBGRVLEFCLK 120
Qy 121 HRSPPGLVLAQGTPTNRTVCKRCPDGFPSGETSSKAPCRKHTNCSLGLLLIQGNAT 180
Db 121 HRSPPGLVLAQGTPTNRTVCKRCPDGFPSGETSSKAPCRKHTNCSLGLLLIQGNAT 180
Qy 181 HDNVCNGREATONCGIDVTLCCEAFAFFFAVPTKII PNWLSVLDLSLPGTKVNAESVERI 240
Db 181 HDNVCNGREATONCGIDVTLCCEAFAFFFAVPTKII PNWLSVLDLSLPGTKVNAESVERI 240
Qy 241 KRRHSSQBTQFOLLKWKHQRNDQEMVKKIIQDIDLCESSVQRHIGHANLTTEQRLILME 300
Db 241 KRRHSSQBTQFOLLKWKHQRNDQEMVKKIIQDIDLCESSVQRHIGHANLTTEQRLILME 300
Qy 301 SLPGKKISPDIERTRKTCPSQQLKLLSLWRIKNGDQDTL KGLMYALKHLKAYHFPKT 360
Db 301 SLPGKKISPDIERTRKTCPSQQLKLLSLWRIKNGDQDTL KGLMYALKHLKAYHFPKT 360
Qy 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 2
US-08-795-445A-2
; Sequence 2, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-2

Query Match 100.0%; Score 2185; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.5e-200;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNKWLCCALLVFLDIIETWTQTTPPKYLYHDPETGROLLCDKCAPGYLYKHCHTVRRKT 60
Db 1 MNKWLCCALLVFLDIIETWTQTTPPKYLYHDPETGROLLCDKCAPGYLYKHCHTVRRKT 60

Qy 61 LCVPCPDYSDTSWHTSDECVYCSVPCKELQTVKQECNRTNHRVCEBGRVLEFCLK 120
Db 61 LCVPCPDYSDTSWHTSDECVYCSVPCKELQTVKQECNRTNHRVCEBGRVLEFCLK 120
Qy 121 HRSPPGLVLAQGTPTNRTVCKRCPDGFPSGETSSKAPCRKHTNCSLGLLLIQGNAT 180
Db 121 HRSPPGLVLAQGTPTNRTVCKRCPDGFPSGETSSKAPCRKHTNCSLGLLLIQGNAT 180
Qy 181 HDNVCNGREATONCGIDVTLCCEAFAFFFAVPTKII PNWLSVLDLSLPGTKVNAESVERI 240
Db 181 HDNVCNGREATONCGIDVTLCCEAFAFFFAVPTKII PNWLSVLDLSLPGTKVNAESVERI 240
Qy 241 KRRHSSQBTQFOLLKWKHQRNDQEMVKKIIQDIDLCESSVQRHIGHANLTTEQRLILME 300
Db 241 KRRHSSQBTQFOLLKWKHQRNDQEMVKKIIQDIDLCESSVQRHIGHANLTTEQRLILME 300
Qy 301 SLPGKKISPDIERTRKTCPSQQLKLLSLWRIKNGDQDTL KGLMYALKHLKAYHFPKT 360
Db 301 SLPGKKISPDIERTRKTCPSQQLKLLSLWRIKNGDQDTL KGLMYALKHLKAYHFPKT 360
Qy 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 3
US-08-795-447A-2
; Sequence 2, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-447A-2

Query Match 100.0%; Score 2185; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.5e-200;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNKWLCCALLVFLDIIETWTQTTPPKYLYHDPETGROLLCDKCAPGYLYKHCHTVRRKT 60
Db 1 MNKWLCCALLVFLDIIETWTQTTPPKYLYHDPETGROLLCDKCAPGYLYKHCHTVRRKT 60
Qy 61 LCVPCPDYSDTSWHTSDECVYCSVPCKELQTVKQECNRTNHRVCEBGRVLEFCLK 120

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 18:47:04 ; Search time 123.333 Seconds
(without alignments)
2293.920 Million cell updates/sec

Title: US-09-718-725A-121

Perfect score: 2185

Sequence: 1 MNKWLCCALLVFLDIIEWTT.....QKLFLFMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 05 80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	100.0	401	1	TR11B_RAT
2	2093	95.8	401	2	Q6P112_MOUSE
3	2079	95.1	401	1	TR11B_MOUSE
4	1914	87.6	401	1	TR11B_HUMAN
5	1909	87.4	401	2	Q53PX6_HUMAN
6	1493.5	68.4	402	2	Q4FPK2_CHICK
7	1010	46.2	387	2	Q6GLN3_XENLA
8	571.5	26.2	480	2	Q4SH87_TETNG
9	553	25.3	146	2	Q7ZZY4_CHICK
10	437	20.0	186	2	Q7ZZY4_CHICK
11	425.5	19.5	300	1	TNR6B_HUMAN
12	406.5	18.6	286	2	Q6RW61_BRARE
13	386.5	17.7	302	2	Q9PUS0_SALPO
14	382	17.5	285	2	Q90W71_ONCMY
15	376	17.2	285	2	Q90Y56_ONCMY
16	348.5	15.9	637	2	Q5TVN2_BRARE
17	325	14.9	561	2	Q4SH86_TETNG
18	323	14.8	459	2	Q63227_MOUSE
19	322	14.7	474	1	TNR1B_MOUSE
20	322	14.7	474	2	Q545P4_MOUSE
21	320	14.6	461	1	TNR1B_HUMAN
22	320	14.6	461	2	Q5THJ6_HUMAN
23	315	14.4	651	2	Q98SM6_CHICK
24	312	14.3	461	2	Q6VU8_RAT
25	312	14.3	474	1	TNR1B_RAT
26	312	14.3	474	2	Q5YLPO_RAT
27	304.5	13.9	655	1	TNR21_HUMAN
28	295.5	13.5	655	1	TNR21_MOUSE
29	295.5	13.5	655	2	Q543Y9_MOUSE
30	292	13.4	433	2	Q912M6_RAT
31	278	12.7	463	2	Q4RF28_TETNG

32	277.5	12.7	625	1	TNR11_MOUSE
33	275	12.6	321	2	Q59EP9_HUMAN
34	274	12.5	457	2	Q81VS6_HUMAN
35	274	12.5	616	1	TNR11_HUMAN
36	273.5	12.5	467	2	Q800I0_CHICK
37	272	12.4	289	1	TNR5_MOUSE
38	272	12.4	289	2	Q542B1_MOUSE
39	272	12.4	289	2	Q8K2X6_MOUSE
40	270	12.4	289	2	Q4QW2_RAT
41	267.5	12.2	462	2	Q805B0_CHICK
42	267.5	12.2	462	2	Q5ZL08_CHICK
43	266	12.2	483	2	Q800K7_PAROL
44	263	12.0	223	2	Q86YK5_HUMAN
45	263	12.0	277	1	TNR5_HUMAN

ALIGNMENTS

RESULT 1

ID TR11B_RAT STANDARD; PRT; 401 AA.
AC C08727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
(Osteoprotegerin).
DE (Osteoprotegerin).
GN Name=Tnfrsf1b; Synonyms=Opg;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
Cell 89:309-319(1997).
[2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]

TISSUE=Lung;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
its function in osteoclastogenesis. Inhibits the activation of
osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
seems to depend on the local RANKL/OPG ratio. May also play a role
in preventing arterial calcification. May act as decoy receptor
for TRAIL and protect against apoptosis. TRAIL binding blocks the
inhibition of osteoclastogenesis (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- INDUCTION: Up-regulated by osteopontin.
CC -!- SIMILARITY: Contains 2 death domains.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; U94330; AA853707.1; -; mRNA.
DR EMBL; BC081830; AA81830.1; -; mRNA.

```

DR HSP; P19438; INCF.
DR Ensembl; ENSRN00000008336; Rattus norvegicus.
DR RGD; 619802; Tnfrsf11b.
DR GO; GO:0045779; P:negative regulation of bone resorption; IMP.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . ; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1. _c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Apoptosis; Cytokine; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT REPEAT 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT CARBOHYD 98 98
FT CARBOHYD 155 155
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
SQ SEQUENCE 401 AA; 46192 MW; FEGCA31FD4E573A CRC64;

Query Match 100.0%; Score 2185; DB 1; Length 401;
Best Local Similarity 100.0%; Pred. No. 7e-151;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 LCVPCPDYSYTDSWHTSDECVYCSVPCKELQTVKQECNRTNHRVCECEBGRYLELEFCLK 120

QY 121 HRSPPGLVGLVLAQTPERTNTVCKRCPDGFSGSETSKAPCRKHTNCSSLLGLLIQKGNAT 180
DB 121 HRSPPGLVGLVLAQTPERTNTVCKRCPDGFSGSETSKAPCRKHTNCSSLLGLLIQKGNAT 180

QY 181 HDNVCSGNREATQNGIDVTLCCEAFFRPAVPTKIIPNWSLVLDSPGTVKNASVERI 240
DB 181 HDNVCSGNREATQNGIDVTLCCEAFFRPAVPTKIIPNWSLVLDSPGTVKNASVERI 240

QY 241 KRHSQQQTQFOLLKWKHQRDQBWVKIIQDIDLCESSVQRHGHANLTTEQLRIIME 300
DB 241 KRHSQQQTQFOLLKWKHQRDQBWVKIIQDIDLCESSVQRHGHANLTTEQLRIIME 300

QY 301 SLPGKKISPDEIERTRKTKPSEQLKLLSLRWIRKNGQDQTLKGLMYALKHLKAYHFPKT 360
DB 301 SLPGKKISPDEIERTRKTKPSEQLKLLSLRWIRKNGQDQTLKGLMYALKHLKAYHFPKT 360

QY 361 VTHSLRKTIIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTHSLRKTIIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 2
Q6P112 MOUSE
ID Q6P112_MOUSE PRELIMINARY; PRT; 401 AA.
AC Q6P112;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 11b
DE (Osteoprotegerin).
DE Name=Tnfrsf11b;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
TISUE=Limb;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISUE=Limb;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049782; AAH49782.1; -, mRNA.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0042489; P:negative regulation of ontogenesis (sensu. . ; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 401 AA; 45965 MW; 7C708B52EB46BA0E CRC64;

Query Match 95.8%; Score 2093; DB 2; Length 401;
Best Local Similarity 95.0%; Pred. No. 3.6e-144;
Matches 381; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVFLDIIIEWTTQTETPPPKYLHYDPETGROLLCDKCAPGYLKHQCHTVRRKT 60
DB 1 MNKWLCCALLVFLDIIIEWTTQTETPPPKYLHYDPETGROLLCDKCAPGYLKHQCHTVRRKT 60

QY 61 LCVPCPDYSYTDSWHTSDECVYCSVPCKELQTVKQECNRTNHRVCECEBGRYLELEFCLK 120
DB 61 LCVPCPDYSYTDSWHTSDECVYCSVPCKELQTVKQECNRTNHRVCECEBGRYLELEFCLK 120

```


GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 18:46:34 ; Search time 115.667 Seconds
(without alignments)
1523.264 Million cell updates/sec

Title: US-09-718-725A-121
Perfect score: 2185
Sequence: 1 MKWLCCALLVFLDIIEWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003s:*
7: Geneseqp2003Bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2185	100.0	401	2 AAW38343	Aaw38343 Rat osteo
2	2185	100.0	401	4 Aab66974	Aab66974 Rat OPG.
3	2185	100.0	401	8 Adm28809	Adm28809 Rat osteo
4	2185	100.0	401	9 Aeb19867	Aeb19867 Rat osteo
5	2177	99.6	401	9 Aeb19804	Aeb19804 Osteoprot
6	2079	95.1	401	2 AAW38344	Aaw38344 Mouse ost
7	2079	95.1	401	4 AAB80898	Aab80898 Human ost
8	2079	95.1	401	4 AAY72916	Aay72916 Human ost
9	2079	95.1	401	4 AAB66975	Aab66975 Murine OP
10	2079	95.1	401	8 Adm28811	Adm28811 Mouse ost
11	2079	95.1	401	9 AEB19866	Aeb19866 Murine os
12	2064	94.5	401	9 AEB19806	Aeb19806 Osteoprot
13	1965	89.9	380	4 AAB66987	Aab66987 Human OPG
14	1965	89.9	380	8 Adm28826	Adm28826 Mouse ost
15	1965	89.9	380	9 AEB19855	Aeb19855 Osteoprot
16	1960	89.7	380	8 Adm28861	Adm28861 Mouse ost
17	1914	87.6	401	2 AAY05742	Aay05742 Tumour ne
18	1914	87.6	401	2 AAW95030	Aaw95030 Tumour ne
19	1914	87.6	401	2 AAW83926	Aaw83926 Human FTH
20	1914	87.6	401	3 AAB18715	Aab18715 A human t
21	1914	87.6	401	4 AAB60570	Aab60570 Human TNF
22	1914	87.6	401	6 AAB36245	Aab36245 Human TRA
23	1914	87.6	401	6 AAO31135	Aao31135 Human TRA
24	1914	87.6	401	7 ADD01625	Add01625 Human ost

25	1914	87.6	401	7 ADF16158	Adf16158 Human alb
26	1914	87.6	401	7 ADF16153	Adf16153 Human alb
27	1914	87.6	401	7 ADF16151	Adf16151 Human alb
28	1914	87.6	401	7 ADF15231	Adf15231 Human alb
29	1914	87.6	401	7 ADF16152	Adf16152 Human alb
30	1914	87.6	401	7 ADF16154	Adf16154 Human alb
31	1914	87.6	401	7 ADF16155	Adf16155 Human alb
32	1914	87.6	401	7 ADF16156	Adf16156 Human alb
33	1914	87.6	401	7 ADF15230	Adf15230 Human alb
34	1914	87.6	401	7 ADF15244	Adf15244 Human alb
35	1914	87.6	401	7 ADF16157	Adf16157 Human alb
36	1914	87.6	401	8 AdR82154	AdR82154 Human TRA
37	1914	87.6	401	9 ADY34172	Ady34172 Human TRA
38	1914	87.6	401	9 AEA27537	Aea27537 Human TRA
39	1914	87.6	401	9 AEA55153	Aea55153 Human TRA
40	1914	87.6	401	9 AEB19868	Aeb19868 Human ost
41	1914	87.6	986	7 ADF15016	Adf15016 Human alb
42	1914	87.6	986	7 ADF15030	Adf15030 Human alb
43	1909	87.4	401	2 AAR99925	Aar99925 Full leng
44	1909	87.4	401	2 AAW53239	Aaw53239 Human OCI
45	1909	87.4	401	3 AAY88622	Aay88622 Osteoclas

ALIGNMENTS

RESULT 1

AAW38343
ID AAW38343 standard; protein; 401 AA.

XX AC AAW38343;

XX DT 20-APR-1998 (first entry)

XX DE Rat osteoprotegerin.

XX KW Rat; osteoprotegerin; antibody; diagnosis; affinity purification;
KW recombinant production; transgenic animal; treatment; prevention;
KW antisense oligonucleotide; probe; detection; screening; bone disease;
KW osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;
KW rheumatoid arthritis; osteomyelitis; osteolytic metastasis;
KW periodontal bone loss; bone necrosis; osteopaenia.

XX OS Rattus sp.

XX PN DE19654610-A1.

XX PD 26-JUN-1997.

XX PF 20-DEC-1996; 96DE-01054610.

XX PR 22-DEC-1995; 95US-00577788.

XX FR 03-SEP-1996; 960US-00706945.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;

XX DR WPI; 1997-334271/31.

XX N-PSDB; AAT96061.

XX PT Nucleic acid encoding osteoprotegerin - useful for treatment of diseases

XX PS involving excessive bone loss, e.g. osteoporosis.

XX Claim 23; Page 102-104; 182pp; German.

XX The present sequence is rat osteoprotegerin (OPG). Anti-OPG antibodies
CC can be used in OPG diagnostic assays, and as affinity purification
CC materials. The OPG cDNA can be used to express recombinant OPG and to
CC generate transgenic animals. It can also be used to regulate the level of
CC OPG in mammals, specifically to increase OPG levels, however the use of
CC antisense sequences is also contemplated. Fragments of the cDNA can be
CC used as probes to detect OPG expressing cells and tissue, and to screen

CC cDNA libraries for related sequences. OPG can be used to treat or prevent
 CC bone diseases, specifically excessive bone loss, e.g. osteoporosis,
 CC Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid
 CC arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,
 CC bone necrosis and osteopaenia
 XX
 SQ Sequence 401 AA;

Query Match 100.0%; Score 2185; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 6.8e-183; Indels 0; Gaps 0;
 Matches 401; Conservative 0; Mismatches 0;
 QY 1 MNKWLCCALLVFLDIIIEWTTQETPPPKYLHYDPETGRQLLCKDCAPGYLKQHCIVRRKT 60
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 QY 61 LCVPCPDYSYTDTSWHTSDVCYVCKELQTVKQECNTHNRVCECEGRLYLEFCLK 120
 DB 61 LCVPCPDYSYTDTSWHTSDVCYVCKELQTVKQECNTHNRVCECEGRLYLEFCLK 120
 QY 121 HRSPPGLGLVLAQTPERTVCKRCPDGFSGTSSKAPCRKHTNCSSGLLLIQQGNAT 180
 DB 121 HRSPPGLGLVLAQTPERTVCKRCPDGFSGTSSKAPCRKHTNCSSGLLLIQQGNAT 180
 QY 181 HDNVCNREATQNGCIDVTLCEEAFFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
 DB 181 HDNVCNREATQNGCIDVTLCEEAFFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
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 DB 241 KRRHSSQBTQFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHANLTTEQRLIME 300
 QY 301 SLPGKKISPDERTKTKCPSEQLLKLWLRIKNGQDQTLKGLMYALKHLYKAYHFPKT 360
 DB 301 SLPGKKISPDERTKTKCPSEQLLKLWLRIKNGQDQTLKGLMYALKHLYKAYHFPKT 360
 QY 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 DB 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 2

AAB66974
 ID AAB66974 standard; protein; 401 AA.

AC AAB66974;

DT 19-APR-2001 (first entry)

XX Rat OPG.

XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
 KW ischaemia; Parkinson's disease.

XX Rattus sp.

XX WO200103719-A2.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-US018657.

XX 09-JUL-1999; 99US-00350670.

XX 09-DEC-1999; 99US-00457647.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Sernaldi G;

XX

DR WPI; 2001-103031/11.

XX N-PSDB; AAF57836.

PT Treating conditions leading to bone loss such as rheumatoid arthritis,
 PT multiple sclerosis and asthma, comprises administering an osteoprotegerin
 PT protein in conjunction with e.g. inhibitors of interleukin and tumor
 PT necrosis factor alpha.
 PT

XX Disclosure; Fig 2; 316pp; English.

XX The present invention relates to a method for treating conditions leading
 CC to bone loss. The method comprises administering a purified and isolated
 CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
 CC in conjunction with other substances such as tumour necrosis factor-alpha
 CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
 CC modulators, fibroblast growth factor (FGF)-10 modulators and/or platelet
 CC activating factor (PAF) antagonists. The method is useful for treating
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
 CC graft-versus-host disease (GvHD). Other diseases that can be treated
 CC include acute pancreatitis, Alzheimer's disease, anorexia,
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 CC psoriasis and septic shock
 XX

SQ Sequence 401 AA;

Query Match 100.0%; Score 2185; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 6.8e-183;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNKWLCCALLVFLDIIIEWTTQETPPPKYLHYDPETGRQLLCKDCAPGYLKQHCIVRRKT 60
 DB 1 MNKWLCCALLVFLDIIIEWTTQETPPPKYLHYDPETGRQLLCKDCAPGYLKQHCIVRRKT 60
 QY 61 LCVPCPDYSYTDTSWHTSDVCYVCKELQTVKQECNTHNRVCECEGRLYLEFCLK 120
 DB 61 LCVPCPDYSYTDTSWHTSDVCYVCKELQTVKQECNTHNRVCECEGRLYLEFCLK 120
 QY 121 HRSPPGLGLVLAQTPERTVCKRCPDGFSGTSSKAPCRKHTNCSSGLLLIQQGNAT 180
 DB 121 HRSPPGLGLVLAQTPERTVCKRCPDGFSGTSSKAPCRKHTNCSSGLLLIQQGNAT 180
 QY 181 HDNVCNREATQNGCIDVTLCEEAFFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
 DB 181 HDNVCNREATQNGCIDVTLCEEAFFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
 QY 241 KRRHSSQBTQFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHANLTTEQRLIME 300
 DB 241 KRRHSSQBTQFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHANLTTEQRLIME 300
 QY 301 SLPGKKISPDERTKTKCPSEQLLKLWLRIKNGQDQTLKGLMYALKHLYKAYHFPKT 360
 DB 301 SLPGKKISPDERTKTKCPSEQLLKLWLRIKNGQDQTLKGLMYALKHLYKAYHFPKT 360
 QY 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 DB 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 3

ADM28809

ID ADM28809 standard; protein; 401 AA.

XX AC ADM28809;

XX DT 20-MAY-2004 (first entry)

XX Rat osteoprotegerin, OPG.

XX